

























17	em_est pl 17	17
18	em_est pl 18	18
19	em_est pl 19	19
20	em_est pl 20	20
21	em_est pl 21	21
22	em_est pl 22	22
23	em_est pl 23	23
24	em_est pl 24	24
25	em_est pl 25	25
26	em_est pl 26	26
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98	em_est pl 98	98
99	em_est pl 99	99
100	em_est pl 100	100

190: qb qss 25: \*

191: qb qss 26: \*

192: qb qss 27: \*

193: qb qss 28: \*

pred., No. is the number of results predicted by relative to have a score greater than or equal to the score of the result being pointed, and is derived by analyzing the total score distribution.

## SUMMARY

Result No.	Score	Query Match	Length	MB	TD	Postscript
1	251.2	92.6	486	12	AA049214	AA049214 ESF191001
2	182.4	64.7	583	96	AW914510	AW914510 nt154008.7
3	182.4	64.7	710	109	BE545105	BE545105 G01206020
4	182.4	64.7	645	16	A1114976	A1114976 nt141001.7
5	182	64.5	929	29	AA0051342	AA0051342 AA0051342
6	181.4	64.5	648	7	AA046427	AA046427 G0004101.2
7	181.4	64.5	598	147	W06873	W06873 nt194003.1
8	181.4	64.5	665	147	W06821	W06821 nt194008.1
9	181.4	64.5	750	87	AW213226	AW213226 nt011109.7
10	180.8	64.1	522	26	A1393572	A1393572 nt166401.7
11	180.8	64.1	651	2	AA097695	AA097695 nt015101.0
12	180.8	64.1	803	29	A10080764	A10080764 AA0007044
13	180.8	64.1	825	29	A10079797	A10079797 AA0079797
14	180.6	64.0	671	9	AA59242	AA59242 G0224006.1
15	180.4	64.0	495	108	BE348424	BE348424 nt180005.7
16	179.8	63.8	416	48	AW243256	AW243256 nt000109.7
17	179.8	63.8	804	29	A10080239	A10080239 AA0007044
18	179.6	63.7	510	11	AA771176	AA771176 nt186095.1
19	179.2	63.5	528	111	BE5551074	BE5551074 nt118010
20	179.2	63.4	407	88	AW257556	AW257576 nt154004.7
21	178.4	63.3	523	109	BE555226	BE555226 nt143104.7
22	178.4	63.3	636	87	AW229547	AW229547 nt009604.7
23	177.6	63.0	825	29	AA079644	AA079644 AA079644
24	176.8	62.7	342	6	AA039556	AA039556 nt153003.1
25	176.4	62.6	436	89	AW207410	AW207410 nt229005.7
26	175.2	62.1	490	10	AA652114	AA652114 nt256005.1
27	174.4	61.5	815	29	AA062155	AA062155 nt007105.1
28	174.4	61.5	877	29	AA062108	AA062108 AA0051308
29	174.4	61.5	908	147	BE5916871	BE5916871 nt16604009
30	172.6	61.2	520	10	AA688728	AA688728 nt23402.1
31	172.4	61.1	644	4	AA021466	AA021466 nt25612.1
32	172.4	61.1	768	29	AA035650	AA035650 nt000000.7
33	171.8	60.9	588	109	BE5554309	BE5554309 nt000000.7
34	170.8	60.6	308	138	BE5986446	BE5986446 nt118003.1
35	170.4	60.4	563	9	AA598669	AA598669 nt021603.1
36	169.2	60.0	299	138	BE5987318	BE5987318 nt118003.1
37	167.4	59.4	480	29	AA036012	AA036012 AA0006020
38	166.2	58.9	601	196	BE291451	BE291451 nt16004066
39	166.2	58.9	630	14	AA5210085	AA5210085 nt254005.1
40	166.2	58.9	636	106	BE500681	BE500681 nt01104045
41	166	58.9	815	29	AA051277	AA051277 AA0051304
42	165.2	58.6	714	110	BE597483	BE597483 nt152412.1
43	164.4	58.3	514	8	AA579897	AA579897 nt214001.7
44	164.4	58.3	519	10	AA554480	AA554480 nt007002.7
45	159.4	56.5	924	29	AA076072	AA076072 AA007002

[illegible][illegible]













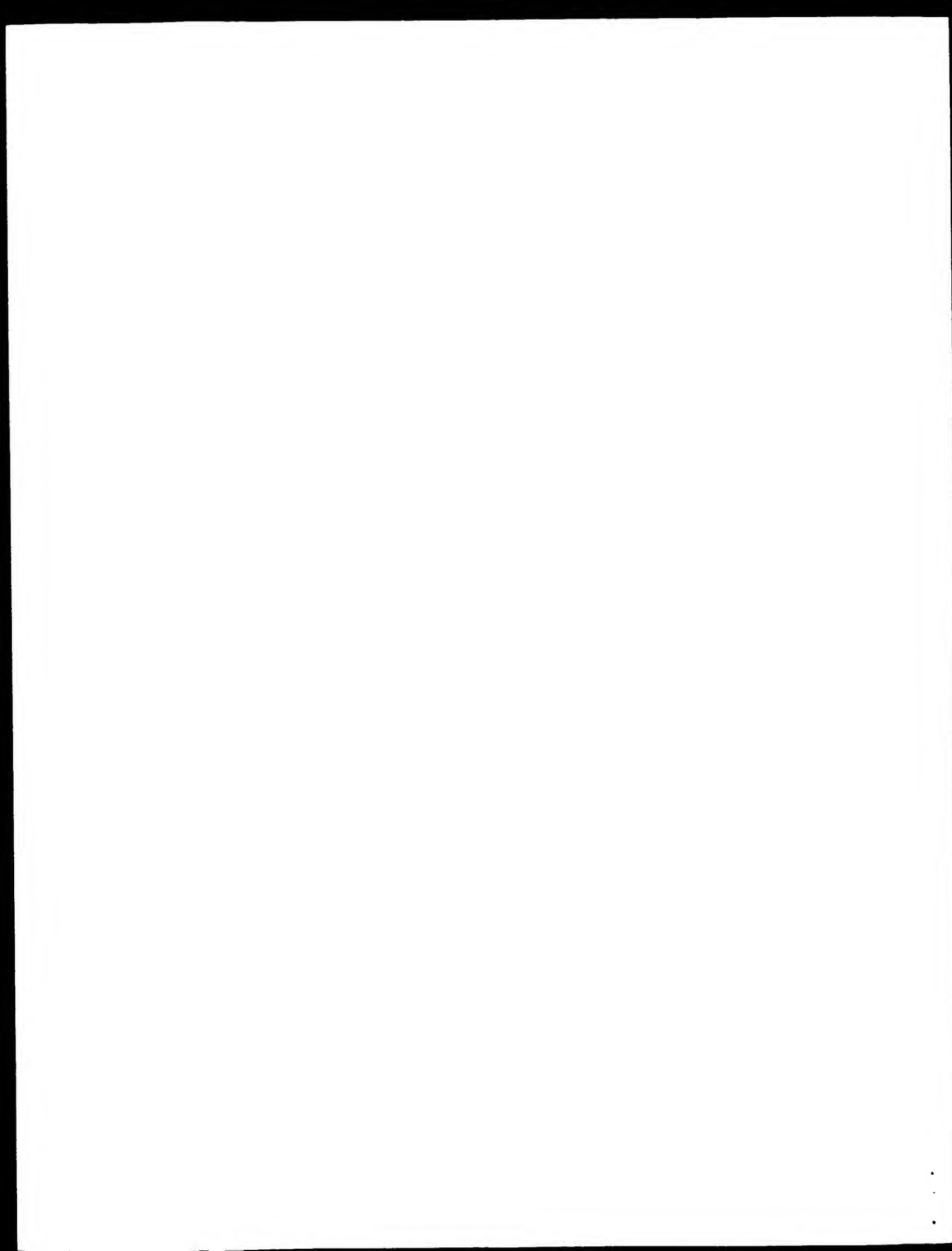












GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2001, 17:53:19 : Search time 4464.91 Seconds  
(without alignments)  
299.162 Million cell updates/sec

Title: us-09-490-609b-318

Perfect score: 261

Sequence: 1 aaaaagaagaatcaatgaa.....taagctctattataaaca 261

Scoring table: IDENTITY\_NOC  
Gapop 10.0 , Gapext 1.0

Searched: 118134 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 250000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenBank:

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_om:\*  
4: gb\_ov:\*  
5: gb\_ph:\*  
6: gb\_ph1:\*  
7: gb\_ph2:\*  
8: gb\_pr1:\*  
9: gb\_pr2:\*  
10: gb\_pr3:\*  
11: gb\_ro:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: em\_hun:\*  
15: em\_hum1:\*  
16: em\_hum2:\*  
17: em\_in:\*  
18: em\_om:\*  
19: em\_or:\*  
20: em\_ov:\*  
21: em\_pat:\*  
22: em\_ph:\*  
23: em\_ph1:\*  
24: em\_ro:\*  
25: em\_sts:\*  
26: em\_sy:\*  
27: em\_un:\*  
28: em\_vl:\*  
29: gb\_ha1:\*  
30: gb\_ha2:\*  
31: gb\_in1:\*  
32: gb\_in2:\*  
33: gb\_ba1:\*  
34: gb\_ba2:\*  
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37: gb\_pr4:\*  
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39: gb\_ha2:\*  
40: gb\_ha3:\*  
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43: gb\_ha6:\*  
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59: gb\_ha10:\*  
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62: em\_ha3:\*  
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64: em\_hum6:\*  
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66: gb\_ha2:\*  
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68: gb\_ha4:\*  
69: gb\_ha5:\*  
70: gb\_ha6:\*  
71: gb\_ha7:\*  
72: gb\_ha8:\*  
73: gb\_ha9:\*  
74: em\_ha1:\*  
75: em\_ha2:\*  
76: em\_ha3:\*  
77: gb\_ha1:\*  
78: gb\_ha2:\*  
79: gb\_ha3:\*  
80: gb\_ha4:\*  
81: gb\_ha5:\*  
82: gb\_ha6:\*  
83: em\_ha1:\*  
84: gb\_ha2:\*  
85: gb\_ha3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	OP	IP	Description
1	253.6	97.2	1594	11	RIEM-2A	X69621 R. norvegicus
2	253.6	97.2	1605	11	AB037934	AB037934 Rattus norvegicus
3	253.6	97.2	6125	11	PATP50P	U14622 P. patens
4	252	96.6	1594	11	KAT-3P1	U28457 Kat mRNA to
5	139	49.8	1573	11	EM028947	U28457 Mus musculus
6	87.6	33.6	1216	21	EM028947	EM028947 Mus musculus
7	67.4	25.8	1109	11	U86217	U86217 Mus musculus
8	40.6	15.6	96258	67	AL161729	AL161729 Homo sapi
9	40.6	15.6	120314	37	AL133338	AL133338 Human DNA
10	40.6	15.6	171777	68	AL56122	AL56122 Homo sapi
11	40	15.3	1394	3	AB035446	AB035446 Bos taurus
12	40	15.3	14499	1	AL002123	AL002123 H. sapi
13	38.8	14.9	172027	52	AC026090	AC026090 Homo sapi
14	38.4	14.7	105891	8	AC004850	AC004850 Homo sapi
15	38.4	14.7	191956	42	AC018911	AC018911 Homo sapi
16	38.2	14.6	177575	57	AC064846	AC064846 Homo sapi
17	38	14.6	70644	57	AC068593	AC068593 Homo sapi
18	38	14.6	154524	38	AC011660	AC011660 Homo sapi
19	38	14.6	199987	53	AC026982	AC026982 Homo sapi
20	37.8	14.5	180534	53	AC026759	AC026759 Homo sapi
21	37.6	14.4	145888	58	AC073219	AC073219 Homo sapi































```

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Note="assembly_fragment"
misc_feature      11761..21597
Note="assembly_fragment"
misc_feature      21598..35794
Note="assembly_fragment"
misc_feature      35895..50658
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misc_feature      98843..146585
Note="assembly_fragment"
misc_feature      146686..191956
Note="assembly_fragment"
clone_end:17
vector_side:right"

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BASE COUNT 63589 a 32910 c 31618 g 62938 t 501 others

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Query Match      14.7% Score 48.4; DB 42; Length 191956;
Best Local Similarity 49.7%; Pred. No. 13;
Matches 96; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 11 aatcaatgaattttcaatcttttttttttaataaqaqaactataattataqaatgaattaaa 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 104605 AAAAAATTATATTTTAAATGATATAAAATAAATCAATGATATCTGTATTTCAATATAA 104945

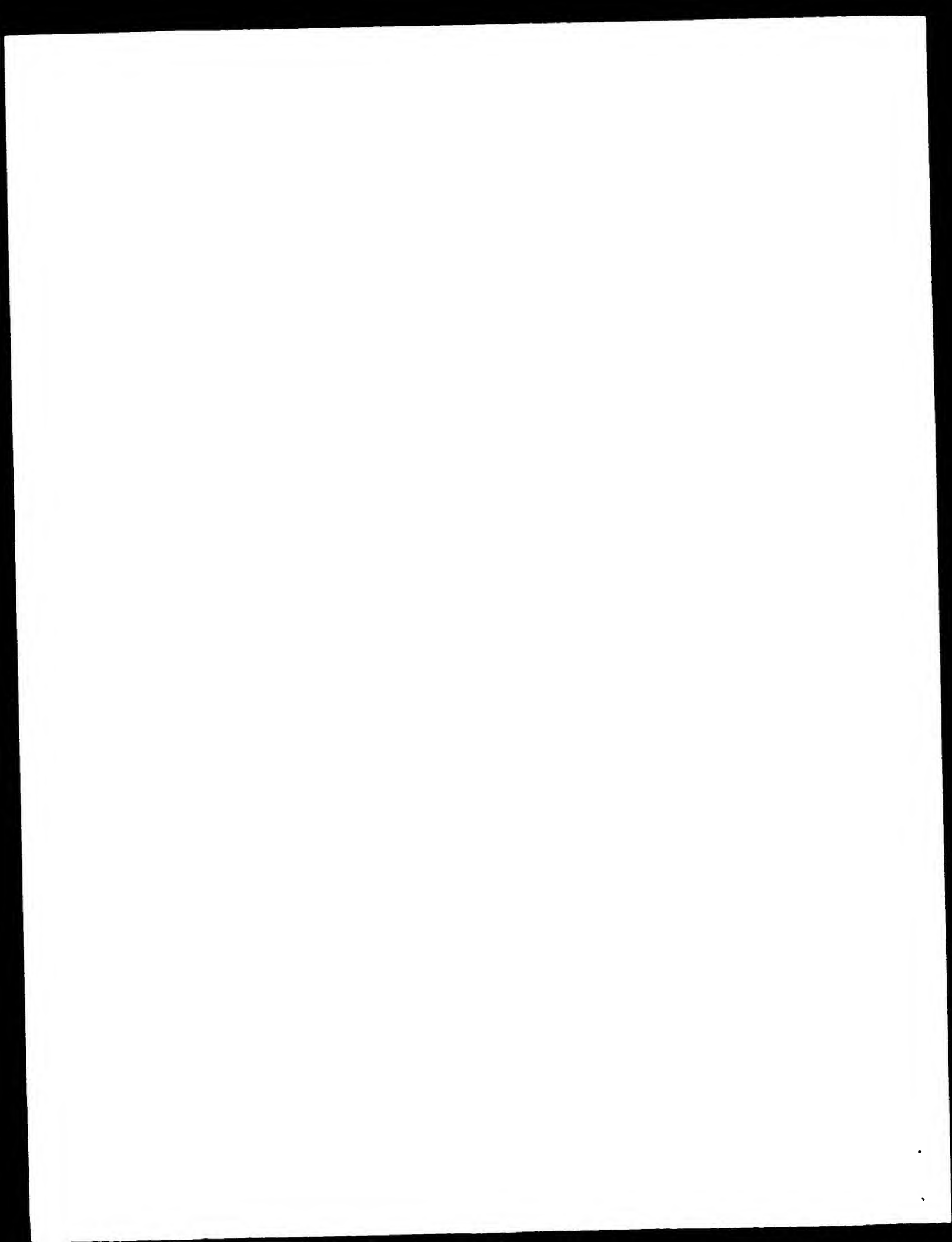
QY 71 ctggttaattkacacttttgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10945 AAAAAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 109866

QY 131 atdaaaacatataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103885 AAGAAGATAGATGTCACACACAAATTCACAAATGAGAAATGTAATTAAGAGACATTTTAA 103826

QY 191 aaattgaattatt 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103825 AAGAAAGTAAATTT 103813

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Search completed: April 11, 2001, 17:55:23  
Job time: 14185 sec





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121: em\_est1620:\*

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124: em\_est1623:\*

125: em\_est1624:\*

126: em\_est1625:\*

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181: em\_est1680:\*

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183: em\_est1682:\*

184: em\_est1683:\*

185: em\_est1684:\*

186: em\_est1685:\*

187: em\_est1686:\*

188: em\_est1687:\*

189: em\_est1688:\*

191: qb\_48826:\*

192: qb\_48827:\*

193: qb\_48828:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	144.2	51.0	710	25	A1787293	A1787293 q108113.8
2	142.2	50.7	773	16	A1118689	A1118689 m094113.8
3	142.2	50.7	773	16	A1118689	A1118689 m094113.8
4	140	49.8	552	18	A1265242	A1265242 q194113.8
5	140	49.8	552	18	A1265242	A1265242 q194113.8
6	138	49.8	566	15	A1046281	A1046281 m094005.8
7	128.4	49.2	749	17	A1173524	A1173524 m094113.8
8	126.8	48.6	746	25	A1786989	A1786989 q135411.8
9	125.6	47.4	531	17	A1173523	A1173523 m094113.8
10	125.6	47.4	531	17	A1173523	A1173523 m094113.8
11	120.4	46.1	815	17	A1194700	A1194700 q156411.8
12	118.6	45.4	506	25	A1786805	A1786805 q138412.8
13	118.6	45.4	532	17	A1194818	A1194818 q17402.8
14	117.6	45.1	519	40	AW111406	AW111406 M11699.00
15	117.6	45.1	519	40	AW111406	AW111406 M11699.00
16	114	44.3	805	25	A1789754	A1789754 q154008.8
17	102.2	42.5	468	4	AA244771	AA244771 m095400.1
18	97.8	42.5	506	17	A1175922	A1175922 m094005.8
19	96.8	42.1	464	25	A1787307	A1787307 q104405.8
20	87	41.3	456	4	AA255065	AA255065 m074002.1
21	87	41.3	456	4	AA255065	AA255065 m074002.1
22	86.2	41.3	456	4	AA255065	AA255065 m074002.1
23	84.4	40.8	432	16	AA269448	AA269448 q194113.8
24	83.6	40.8	432	16	AA269448	AA269448 q194113.8
25	80.4	40.8	498	29	AV028322	AV028322 AV028322
26	68.8	26.4	405	17	A1195266	A1195266 m074008.8
27	52	19.9	370	17	A1182595	AA243431 m013402.1
28	51.2	19.6	341	3	AA212429	AA243431 m013402.1
29	46.8	17.9	341	3	AA212429	AA243431 m013402.1
30	46.6	17.9	341	3	AA212429	AA243431 m013402.1
31	41.2	15.8	768	13	AA859661	AA859661 q155402.1
32	40.6	15.6	664	29	AA859661	AA859661 q155402.1
33	40.6	15.6	664	29	AA859661	AA859661 q155402.1
34	40.4	15.3	827	190	CNS000013	A1091448 m094113.8
35	40	15.3	827	190	CNS000013	A1091448 m094113.8
36	40	15.3	827	190	CNS000013	A1091448 m094113.8
37	37.8	14.5	811	190	CNS000013	A1091448 m094113.8
38	37.6	14.4	408	149	AA090757	A1741521 m021008.8
39	37.6	14.4	429	17	A1259608	A1741521 m021008.8
40	37.4	14.3	765	27	A1789446	A1789446 m094113.8
41	37.2	14.3	448	24	AA1753791	AA1753791 q1164105.8
42	37.2	14.3	475	91	AA1753791	AA1753791 q1164105.8
43	37.2	14.3	475	91	AA1753791	AA1753791 q1164105.8
44	37.2	14.3	475	91	AA1753791	AA1753791 q1164105.8
45	37.2	14.3	475	91	AA1753791	AA1753791 q1164105.8

# ALIGNMENTS

RESULT 1

A1787293/

LOCUS 31810 x1 Sudan mouse liver mRNA

DEFINITION IMAGE1924171.37 similar to SW:SMO\_MOUSE\_06474 STENOCERIN MARKER

PROTEIN 40 aa mRNA sequence

ACCESSION A1787293

VERSION A1787293.1

KEYWORDS EST

EST 02 JUL 1999

















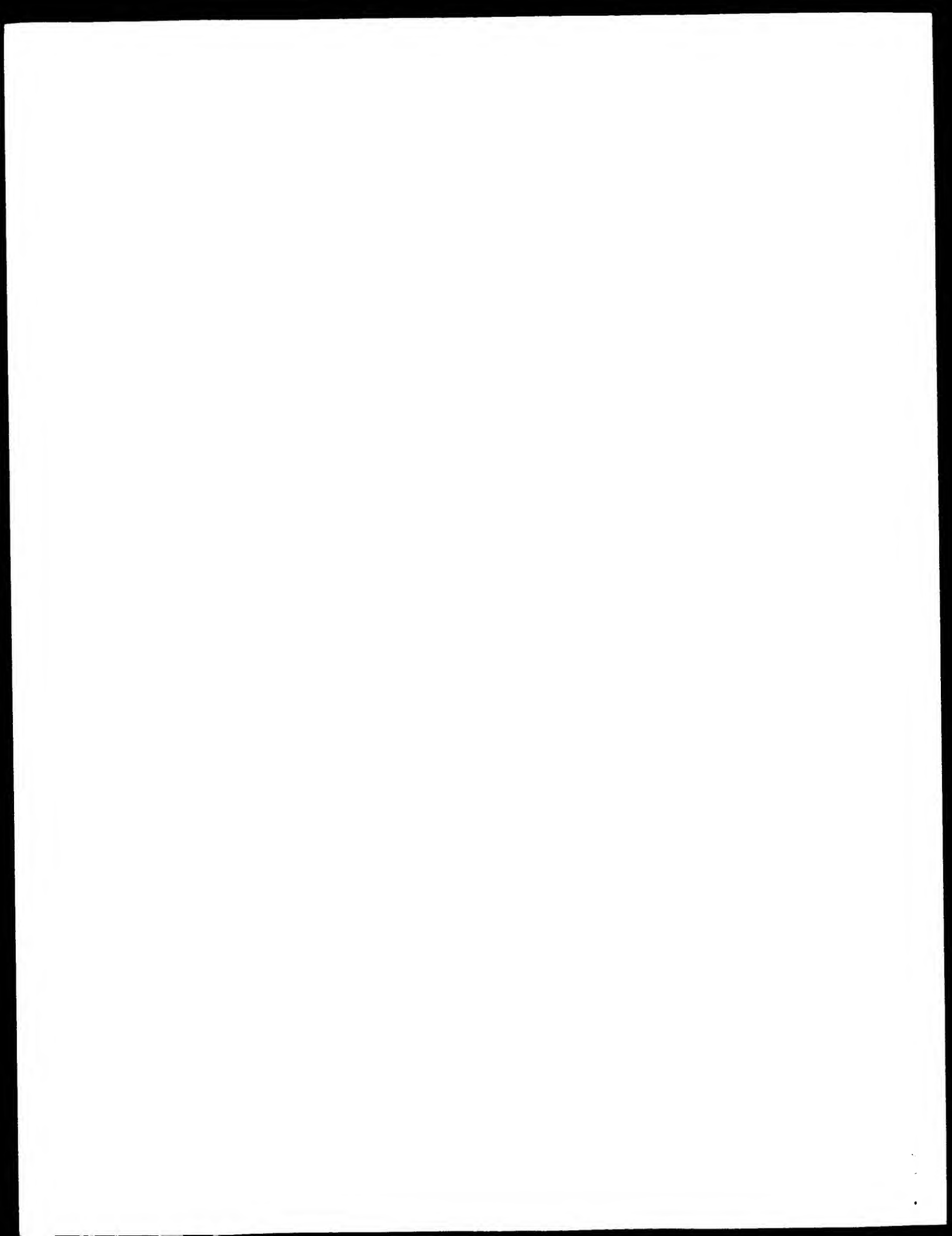


SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
1 (bases 1 to 468)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucuba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Strepov, M., Tan, F., Underwood, K., Moore, B.,  
Theising, R., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, K.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through INL: contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:419062  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 467.

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/lab\_host="DH10B"  
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polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not 1 - oligo(dT) primer [5';  
TCTTACCAATTCAGTCGACCGGCGGCAATCTTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not 1 and cloned into the Not 1  
and Eco RI sites of the modified pTZ19 vector. Library  
constructed and normalized by Bento Soares and M.Fatima  
Ronalds."

BASE COUNT 135 a 73 c 111 q 149 t  
ORIGIN  
Query Match 49.2% Score 102.2; Db 4; Length 468;  
Best local Similarity 78.0%; Pred. NO. 1.2e-16;  
Matches 181; Conservation 3; Mismatches 29; Indels 22; Gaps 4;  
QY 1 aatggaagaatcaatgaatttcaatcttg-tttttttaaagaacatgaatata 59  
Db 257 AAGGAGTCGAAATCAAGAACTTCAATTAGTTTTTTTAAAGAGGTCGATATA 316  
QY 60 gataatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 118  
Db 317 GCAATGTTAA---GCTTAATTAATGATCTTTCATTCGCTCTGGTTGAATAAAGCTAGG 374  
QY 119 catggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 178  
Db 374 CATAGCATATTATGAAGAGTGT-----CATGCTGATTCCTTATT 416  
QY 179 ggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaat 240  
Db 417 TAGAATTTTTAAAGGTGAGAGATTTCCTCCAGAGAAATCAAGAGGTTTTS 468

Search completed: April 11, 2001, 15:40:40  
Job time: 1350.3 sec

































us-09-490-609b-384.rge

Thu Apr 12 10:22:28 2001





TITLE Direct Submission  
 JOURNAL Submitted (on the 1999) Genome Sequencing Center, Washington  
 University, Seattle, WA, U.S.A. 1441 E 1st, 9814 Park St, Seattle, WA, U.S.A.  
 MO 68108, USA  
 COMMENT on Jan 16, 2000 this sequence version replaced nt.7665476.

\*\*\*\*\* Genome Center \*\*\*\*\*  
 \* NOTE: this is a 'working draft' sequence. It currently  
 \* consists of 29 contigs, the true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1314: contig of 1413 bp in length  
 \* 1414: gap of unknown length  
 \* 1414 2619: contig of 1296 bp in length  
 \* 2620 5715: gap of unknown length  
 \* 5715 3887: contig of 1168 bp in length  
 \* 3888 5987: gap of unknown length  
 \* 5988 5295: contig of 1308 bp in length  
 \* 5296 5395: gap of unknown length  
 \* 5396 6572: contig of 1177 bp in length  
 \* 6573 6673: gap of unknown length  
 \* 6673 8101: contig of 1429 bp in length  
 \* 8102 8201: gap of unknown length  
 \* 8202 10076: contig of 1675 bp in length  
 \* 10077 10173: gap of unknown length  
 \* 10173 12439: contig of 2263 bp in length  
 \* 12440 12539: gap of unknown length  
 \* 12540 14893: contig of 2354 bp in length  
 \* 14894 14943: gap of unknown length  
 \* 14943 17495: contig of 2502 bp in length  
 \* 17496 17595: gap of unknown length  
 \* 17596 21723: contig of 4127 bp in length  
 \* 21723 21824: gap of unknown length  
 \* 21824 27619: contig of 5797 bp in length  
 \* 27620 27721: gap of unknown length  
 \* 27721 31491: contig of 4772 bp in length  
 \* 31492 31592: gap of unknown length  
 \* 31592 34601: contig of 3210 bp in length  
 \* 34602 43269: contig of 6368 bp in length  
 \* 43270 43469: gap of unknown length  
 \* 43470 49415: contig of 6046 bp in length  
 \* 49416 49515: gap of unknown length  
 \* 49516 55005: contig of 5490 bp in length  
 \* 55006 62001: contig of 6895 bp in length  
 \* 62002 62101: gap of unknown length  
 \* 62101 69529: contig of 7825 bp in length  
 \* 69530 70029: gap of unknown length  
 \* 70030 80234: contig of 10204 bp in length  
 \* 80234 80334: gap of unknown length  
 \* 80334 90136: contig of 9803 bp in length  
 \* 90137 90236: gap of unknown length  
 \* 90237 99409: contig of 9170 bp in length  
 \* 99410 99507: gap of unknown length  
 \* 99508 110476: contig of 10970 bp in length  
 \* 110477 110577: gap of unknown length  
 \* 110578 122794: contig of 12218 bp in length  
 \* 122795 122895: gap of unknown length  
 \* 122896 134376: contig of 11382 bp in length  
 \* 134377 144777: gap of unknown length  
 \* 144778 145708: contig of 11242 bp in length  
 \* 145709 145809: gap of unknown length  
 \* 145810 161966: contig of 16158 bp in length  
 \* 161967 162066: gap of unknown length  
 \* 162067 180573: contig of 18506 bp in length  
 \* 180574 180673: gap of unknown length  
 \* 180674 200710: contig of 20036 bp in length.

Location/Qualifiers

source 1. 200710  
 /organism="Homo sapiens"  
 /taxid="9606"  
 /chromosome="2"  
 /clone="RP11 469J6"  
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 /note "assembly\_name:Contig46"  
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 /note "assembly\_name:Contig47"  
 2620 3887  
 /note "assembly\_name:Contig48"  
 3888 5295  
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 5296 5395  
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 5396 6572  
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 8102 8201  
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 8202 10076  
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 10174 12439  
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 21724 21824  
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 31593 34601  
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 49506 55005  
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 55006 62000  
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 62001 69529  
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 69530 70030  
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 80335 90136  
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 99410 99507  
 /note "assembly\_name:Contig81"  
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 110578 122794  
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 122795 134376  
 /note "assembly\_name:Contig85"  
 134377 144777  
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 144778 145708  
 /note "assembly\_name:Contig87"  
 145709 161966  
 /note "assembly\_name:Contig88"  
 161967 180572  
 /note "assembly\_name:Contig89"  
 180573 200710  
 /note "assembly\_name:Contig90"  
 200711 2814 others

Query Match 61.7% Score 194.4; DB 4.2; Length 200710;  
 Best Local Similarity 86.3%; Pred. No. 13e-46;  
 M4: 0.55 2.09; Coverage 0; Mismatches 12; Indels 6; Gaps 6;

FEATURES









DB 188853 AAACTTCAGTCCTCCTAAGAGTATAGAGTAAACATGCTCTCTGATATCAAGACGTCG 188794

QY 297 43 296

DB 188794 AA 188792

RESULT 8

AC022942

LOCUS

DEFINITION

AC022942

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

\* This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 1333: contig of 1333 bp in length  
1434 1434: gap of 100 bp  
1434 3122: contig of 1689 bp in length  
3123 3222: gap of 100 bp  
3223 5217: contig of 1995 bp in length  
5218 5317: gap of 100 bp  
5318 8117: contig of 2800 bp in length  
8118 8217: gap of 100 bp  
8218 11179: contig of 2961 bp in length  
11179 11278: gap of 100 bp  
11279 15255: contig of 2977 bp in length  
15256 15355: gap of 100 bp  
15356 18989: contig of 3634 bp in length  
18990 19089: gap of 100 bp  
19090 24048: contig of 4959 bp in length  
24049 24148: gap of 100 bp  
24149 28201: contig of 4053 bp in length  
28202 28301: gap of 100 bp  
28302 33551: contig of 5250 bp in length  
33552 39489: contig of 6338 bp in length  
39490 40089: gap of 100 bp  
40090 45900: contig of 5811 bp in length  
45901 46000: gap of 100 bp  
46001 52633: contig of 6633 bp in length  
52634 52733: gap of 100 bp  
52734 59963: contig of 7231 bp in length  
59965 60064: gap of 100 bp  
60065 69189: contig of 9125 bp in length  
69190 69299: gap of 100 bp  
69299 80935: contig of 11646 bp in length  
80936 81035: gap of 100 bp  
81036 92963: contig of 11929 bp in length  
92965 93064: gap of 100 bp  
93065 107896: contig of 14922 bp in length  
107897 107986: gap of 100 bp  
107987 122024: contig of 14038 bp in length  
122025 122124: gap of 100 bp  
122125 137999: contig of 15875 bp in length  
138000 148099: gap of 100 bp  
148100 154878: contig of 16779 bp in length  
154879 154978: gap of 100 bp  
154979 172428: contig of 17450 bp in length  
172429 172528: gap of 100 bp  
172529 191944: contig of 19416 bp in length.

# FEATURES

Location/Qualifiers  
1..191944  
Genbank "Homo Sapiens"  
chr:1 "Xen:9606"  
Chromosome: "17"  
Map: "17"  
/clone="p11-341p19"  
/clone\_lib="RP11 Human Male BAC"  
1..1333  
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1434..3122  
/note "assembly\_fragment"  
3123..5217  
/note "assembly\_fragment"  
5318..8117  
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8218..11178  
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11279..15255  
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15356..18989  
/note "assembly\_fragment"  
19090..24048  
/note "assembly\_fragment"  
24149..28201  
/note "assembly\_fragment"

Source  
Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: <http://www.mit.edu>  
Contact: Sequencing Submissions@genome.wi.mit.edu  
Project Information  
Center project name: 341P19  
Center clone name: 341P19  
Sequencing vector: M13; M7815; 100% of reads  
Chemistry: dye-terminator Big Dye; 100% of reads  
Assembly program: phrap; version 0.96031  
Consensus quality: 17924 bases at least Q19  
Consensus quality: 15525 bases at least Q19  
Consensus quality: 18823 bases at least Q20  
Insert size: 160000; average 4p  
Insert size: 189744; sum-of-contigs  
Quality coverage: 4.4 in Q20 bases; average 4p  
Quality coverage: 4.4 in Q20 bases; sum of contigs

\* REF: This is a 'working draft' sequence. It currently  
consists of 23 contigs, the true order of the pieces  
is not known, and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.















Genome version 4.5  
Copyright (c) 1993-2000 CompuLink Ltd.

08 nucleotide - nucleotide search, using sw model

Run on: April 11, 2001, 17:56:01 : Search time 4464.91 Seconds  
(without alignments)  
342.719 Million cell updates/sec

Hitset:  
Perfect Score: 299  
Sequence: 1 aactaacattatctctcc.....tctatattgaagatcttgc 299

Scoring Table: IDENTITY 80%  
Gapop 10.0 : Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues 2246266  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenBank.\*  
1: qb\_ba1.\*  
2: qb\_ba2.\*  
3: qb\_om.\*  
4: qb\_ow.\*  
5: qb\_ph.\*  
6: qb\_pi1.\*  
7: qb\_pi2.\*  
8: qb\_pi3.\*  
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14: qb\_pi9.\*  
15: qb\_pi10.\*  
16: qb\_pi11.\*  
17: qb\_pi12.\*  
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38: qb\_pi33.\*  
39: qb\_pi34.\*  
40: qb\_pi35.\*  
41: qb\_pi36.\*  
42: qb\_pi37.\*  
43: qb\_pi38.\*  
44: qb\_pi39.\*  
45: qb\_pi40.\*

44: em\_h1q2.\*  
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141: em\_h1q99.\*  
142: em\_h1q100.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	245	81.9	857	78	HSR115A
2	228.4	76.4	185755	40	AC000501
3	221.2	74.0	215404	68	AL155497
4	221.2	74.0	244977	66	AL148890
5	193.2	64.6	161456	69	AL139153
6	193	64.5	122923	66	AF248376
7	193	64.5	196979	42	AC018746
8	193	64.5	191944	50	AC022950
9	192	64.2	163250	58	AC065217
10	185.2	61.9	168223	49	AC021558
11	184.4	61.7	200710	42	AC019198
12	183.6	61.4	900	85	HMB117
13	183.6	61.4	952	78	HSR115A
14	175.2	58.6	199400	48	CNS0115A
15	169.4	56.7	979	78	HSR115A
16	152.8	51.1	600	65	HMB117A
17	151.2	50.6	143093	66	AF234070
18	146.4	49.0	162703	53	AC027407
19	146.4	49.0	176615	68	AL155142
20	136.6	45.7	61403	54	AC007459
21	131.4	43.9	1350	85	HMB117

















Thu Apr 12 10:22:30 2001

us-09-490-609b-384.rni

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08 nucleic nucleic search, using SW model

Run on: April 11, 2001, 19:47:26 : Search time 191.46 seconds

(without alignments)

251.681 Million cell updates/sec

Hit loc: US-09-490-609b-384

Perfect score: 299

Sequence: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

Score list table: IDENTIFY NUC

Gap: 10.0, GapExt: 1.0

Searched: 280846 seqs, 80540151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum hit seq length: 0

Maximum hit seq length: 20000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database: Issued Patents, NA:\*

1: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

2: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

3: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

4: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

5: 1 nucleic acid (sequence).....1 nucleic acid (sequence) 299

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	96.8	12.3	7218	1	US-08-232-463-14
2	44.8	11.6	2243	1	US-08-145-705A-1
3	32	10.7	2006	3	US-09-079-981-3
4	30.7	10.2	2006	5	US-08-386-3
5	28.8	9.6	1347	3	US-08-622-679C-11
6	28.4	9.5	1346	2	US-08-724-354D-3
7	28.4	9.5	1346	3	US-09-270-984A-3
8	28.2	9.4	704	2	US-08-465-095-15
9	28.2	9.4	992	1	US-08-358-782D-13
10	28.2	9.4	992	2	US-08-764-527A-13
11	28.2	9.4	1383	2	US-08-709-856A-14
12	28.2	9.4	1091	3	US-08-287-375-13
13	28.2	9.4	1462	1	US-08-358-782D-14
14	28.2	9.4	1462	3	US-08-764-527A-14
15	28	9.4	2946	4	US-08-968-563-6
16	28	9.4	2946	4	US-08-969-683A-6
17	27.8	9.3	1020	2	US-08-441-857-5
18	27.8	9.3	1020	4	US-08-193-159-5
19	27.6	9.2	1000	1	US-08-145-705A-4
20	27.6	9.2	862	1	US-08-879-561-6
21	27.6	9.2	14985	1	US-08-652-972A-6
22	27.6	9.2	14985	4	US-08-652-972A-6
23	27	9.0	5613	2	US-08-463-418-1
24	27	9.0	246240	2	US-08-724-394A-20
25	27	9.0	246240	2	US-08-724-394A-21
26	26.8	9.0	53526	4	US-08-724-394A-22
27	26.8	9.0	53526	4	US-08-658-136-2
28	26.8	9.0	53577	4	US-08-658-136-1

29	26.6	8.9	832	1	US-08-430-500A-6
30	26.6	8.9	832	2	US-08-430-500A-6
31	26.6	8.9	1377	1	US-07-940-245-1
32	26.6	8.9	1377	1	US-08-226-486-1
33	26.6	8.9	1729	2	US-08-644-624-1
34	26.6	8.9	1729	2	US-08-716-547-1
35	26.6	8.9	2375	3	US-08-714-918-81
36	26.6	8.9	2407	3	US-08-895-522-2
37	26.6	8.9	3307	3	US-09-195-691-2
38	26.6	8.8	965	5	US-08-06-2
39	26.6	8.8	1785	2	US-08-507-480A-6
40	26.6	8.8	1785	2	US-08-465-809-1
41	26.6	8.8	3810	3	US-08-465-809-1
42	26.6	8.8	3000	1	US-08-184-250A-1
43	26.6	8.8	3000	1	US-08-680-395-1
44	26.6	8.8	3000	4	US-08-06001-1
45	26.6	8.8	5687	2	US-08-480-400A-3

## ALIGNMENTS

RESULT 1

US-08-232-463-14/1

Sequence 14, 561672 hits, US-08-232-463-14

Patent No. 561672

GENERAL INFORMATION:

APPLICANT: TERNER, F.

APPLICANT: SCHULINGER, F.

APPLICANT: TALKNER, F.

TITLE OF INVENTION: RECOMBINANT FLOWEX VIRUS

NUMBER OF INVENTORS: 2

ADDRESS: 1400 11th Ave, Suite 500

ADDRESS: 1400 11th Ave, Suite 500

STATE: VA

COUNTRY: USA

ZIP: 22434-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08-232-463-14

FILING DATE: 26 AUG 1991

CLASSIFICATION: 4-5

PRIOR APPLICATION DATA:

APPLICANT'S NUMBER: 29, 296

FILING DATE: 26 AUG 1991

APPLICANT'S NUMBER: 29, 296

NAME: TERNER, Stephen A.

REGISTRATION NUMBER: 29, 296

REGISTRATION DATE: 29, 296

REGISTRATION DATE: 29, 296

TELEPHONE: (703) 846-9400

TELEFAX: (703) 846-9400

TELEX: 999149

INFORMATION FOR SEQUENCE DATA:

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRAND: SINGLE

Topology: Linear

IMMEDIATE SOURCE:

CLONE: pZap1-15

US-08-232-463-14

Query Match

12.3% Score: 96.8 DB: 1 Length: 7218







































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2	183.2	66.1	278	2	US 08 340 4260-101	Sequence 101, Appl
3	183.2	66.1	278	2	US 08 450 6780-101	Sequence 101, Appl
4	183.2	66.1	278	4	PCT-US95-17111A-101	Sequence 101, Appl
5	33.4	12.1	957	1	US 08 125 746-4	Sequence 4, Appl
6	33.4	12.1	1567	5	US 225 537-3	Patent No. 5225537
7	33.4	12.1	1667	1	US 08 125 745-2	Sequence 2, Appl
8	31.4	11.3	2405	3	US 08 526 136-1	Sequence 1, Appl
9	31.4	11.3	2411	3	US 08 526 136-3	Sequence 4, Appl
10	31.2	11.2	1290	3	US 08 745 977-3	Sequence 4, Appl
11	31.2	11.3	1290	3	US 09 040 699A-4	Sequence 4, Appl
12	30.8	11.1	1741	2	US 08 466 583-1	Sequence 3, Appl
13	30.8	11.1	1741	4	PCT-US95-07820-1	Sequence 1, Appl
14	30.6	11.0	1161	3	US 08 689 421-22	Sequence 1, Appl
15	30.6	11.0	2004	1	US 08 471 033 18	Sequence 22, Appl
16	30.6	11.0	2004	2	US 08 471 034 18	Sequence 18, Appl
17	30.6	11.0	2004	2	US 08 463 483A 18	Sequence 18, Appl
18	30.6	11.0	2004	2	US 08 471 046A 18	Sequence 18, Appl
19	30.6	11.0	2004	2	US 08 470 566B 18	Sequence 18, Appl
20	30.6	11.0	2004	2	US 08 469 334 18	Sequence 18, Appl
21	30.6	11.0	2004	3	US 09 300 529 18	Sequence 13, Appl
22	30.6	11.0	2576	1	US 08 471 033 35	Sequence 35, Appl
23	30.6	11.0	2576	2	US 08 471 034 35	Sequence 35, Appl
24	30.6	11.0	2576	2	US 08 463 483A 35	Sequence 35, Appl
25	30.6	11.0	2576	2	US 08 471 046A 35	Sequence 35, Appl
26	30.6	11.0	2576	2	US 08 470 566B 35	Sequence 35, Appl
27	30.6	11.0	2576	2	US 08 469 334 35	Sequence 35, Appl
28	30.6	11.0	2576	3	US 09 300 529 35	Sequence 35, Appl



us-09-490-609b-465.rst

Thu Apr 12 10:22:37 2001









[illegible]









117: em\_estp16: \*  
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4	242	67.1	42	104	HE127664	HE127664	HE127664
5	240.8	79.7	606	96	AA010455	AA010455	AA010455
6	240.2	79.5	595	1	AA010498	AA010498	AA010498
7	239.2	79.1	575	2	AA144415	AA144415	AA144415
8	238	78.7	290	184	HE126540	HE126540	HE126540
9	237	78.3	529	139	HE016495	HE016495	HE016495
10	236.6	78.2	584	10	AA07875	AA07875	AA07875
11	236.2	78.1	608	13	AA069043	AA069043	AA069043
12	236	78.0	363	87	AA0214669	AA0214669	AA0214669
13	235.4	77.8	506	106	HE342710	HE342710	HE342710
14	209.6	75.7	724	140	AA08590	AA08590	AA08590
15	207.8	75.0	400	28	AL464371	AL464371	AL464371
16	207.4	74.9	520	164	HE138087	HE138087	HE138087
17	205.4	74.2	556	2	AA103617	AA103617	AA103617
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19	205.2	74.1	615	13	AA071237	AA071237	AA071237
20	205	74.0	388	87	AA0214659	AA0214659	AA0214659
21	205	74.0	631	89	AA021586	AA021586	AA021586
22	203.6	73.5	667	186	HE306684	HE306684	HE306684
23	203.6	73.5	107	137	HE343527	HE343527	HE343527
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25	201.2	72.6	656	108	HE409465	HE409465	HE409465
26	201.2	72.6	1138	110	HE573009	HE573009	HE573009
27	200.6	72.4	676	26	AA095511	AA095511	AA095511
28	200.2	72.3	441	156	HE308437	HE308437	HE308437
29	200.2	72.3	540	166	HE409889	HE409889	HE409889
30	200.2	72.2	542	23	AA036474	AA036474	AA036474
31	200	72.2	699	26	AA095447	AA095447	AA095447
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33	199.6	72.1	544	10	AA056250	AA056250	AA056250
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36	199.6	72.1	655	89	AA021208	AA021208	AA021208
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40	199.4	72.0	527	93	AA071840	AA071840	AA071840
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

# ALIGNMENTS

RESULT 1  
 H5202  
 DEFINITION EST10599 Rat p12 cells, RFL treated (7 days) Ratius sp. cDNA  
 clone RFL19 similar to Annexin II, mRNA sequence.  
 EST 02 APR-1998  
 H5202  
 DEFINITION H5202  
 H5202.1 G1:980619  
 EST  
 Ratius sp.

GenCore version 4.5  
Copyright (c) 1993-2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2001, 15:40:57 ; Search time 344.34 Seconds  
(without alignments)  
580.406 Million cell updates/sec

Title: US 09-490-609b 465  
Best hit score: 277  
Sequence: 1 qctctatgagagagagctctctg.....cagatcattaccttcagctta 277

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Sequences: 7901742 seqs, 450474858 residues

Total number of hits satisfying chosen parameters: 15963484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Listing first 45 summaries

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EST :

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- 2: qb\_est2 :
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- 4: qb\_est4 :
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- 116: qb\_est116 :























[illegible]



























Thu Apr 12 10:22:40 2001

us-09-490-609b-488.ini

Page 10

Search completed: April 11, 2001, 19:48:05  
Job time: 18518 sec

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[illegible]

INFORMATION FOR SCHOOL NO. 5  
 "COLUMBIAN" "HARVEST" 1915

INFORMATION FOR SCHOOL NO. 5  
 "COLUMBIAN" "HARVEST" 1915

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1 CORRESPONDENT ADDRESS:
2 ADDRESSEE: NO. 5955348artis Corporation
3 STREET: 4054 Cornwallis Road
4 CITY: Research Triangle Park
5 STATE: NC
6 COUNTRY: USA
7 ZIP: 27709
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: floppy disk
11 COMPUTER: IBM pc compatible
12 OPERATING SYSTEM: PC DOS/MS-DOS
13 SOFTWARE: FASTA in Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/595,977, 536
16 FILING DATE:
17
18 CLASSIFICATION: 435
19
20 ALTERNATE/ADMT INFORMATION:
21 NAME: Molnar, J. Timothy
22 REGISTRATION NUMBER: 48,241
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (919) 541-8587
25 TELEFAX: (919) 541-8689
26
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 10763 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33
34 MOLECULE TYPE: DNA (genomic)
35
36 HYPOTHETICAL: NO
37
38 ANTI-SENSE: NO
39
40 ORIGINAL SOURCE:
41 ORGANISM: Pseudomonas fluorescens
42 STRAIN: GEA9766 (aka M00314 and aka H0915)
43 IMMEDIATE SOURCE:
44 CLONE: Plasmid pB11
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50 OTHER INFORMATION: /product= "methyltransferase"
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53 OTHER INFORMATION: /note= "The first 1000 bases of the E. coli and Mycoplasma genitalium
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72 OTHER INFORMATION: /note= "coli."
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96 OTHER INFORMATION: /product= "Nucleic acid"
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99 OTHER INFORMATION: /note= "sequences, respectively."
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[illegible]





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Stepwise 5, Application no us04040200N
Feature No, 688,264
GENERAL INFORMATION
APPLICANT: California, Thomas D.
APPLICANT: Lane, Stephen T.
APPLICANT: Loper, James M.
APPLICANT: Hill, David S.
APPLICANT: Smith, Jeffrey L.
APPLICANT: Howell, Charles R.
APPLICATION: Insect, Tobacco
TITLE OF INVENTION: New Activation Element
NUMBER OF SEQUENCE: 9
CORRESPONDENT ADDRESS:
ADDRESSOR: CHA DELLY Corporation
STREET: Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10542
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING TIME for compilation:
OPERATING SYSTEM: PC DOS/MR DOS
SOFTWARE: Patent to be used #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/44.0,298
FILING DATE: 02 JUN 1995
CLASSIFICATION: G 06
PRIORITY APPLICATION DATA
APPLICATION NUMBER: US 08/297,442
FILING DATE: 08 AUG 1994
APPLICATION NUMBER: US 08/207,646
FILING DATE: 01 JUL 1994
PRIORITY APPLICATION DATA
APPLICATION NUMBER: US 07/908,284
FILING DATE: 02 JAN 1992
PRIORITY APPLICATION DATA
APPLICATION NUMBER: US 07/540,184
FILING DATE: 08 AUG 1990
ALTERNATIVE TO GENERAL
NAME: Ethanol, Lower Saccharide
REGISTRATION NUMBER: 46,129
REFERENCE: EPO PAGES: 1-5; FIGS 1-14
TELECOMMUNICATION INFORMATION
TELEPHONE: 919 541 8044
TELEFAX: 919 541 8099
INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDDIRECTION: single
TOPOLGNY: linear
MULTIPLE TYPE: DNA (genomic)
HYDRETICAL: N
ANTI SENSE: N
ORIGINAL SOURCE:
ORGANISM: Psychodinus Throscovus
STRAIN: CNA/546
INDIVIDUAL LOCATOR: % 6 kb Ford model restriction
INDIVIDUAL LOCATOR: treatment
IMMEDIATE SOURCE:
CLONE: pT4107
FEATURE:
NAME/KEY: insect location
LOCATION: 210, 1698
OTHER INFORMATION: "off" 1, transferred left to
FEATURE:
NAME/KEY: insect location
LOCATION: 1906, 3044

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[illegible]







PI foodstuffs, and for industrial prodn. of trehalose

XX Claim 1: Page 118-120; 156pp; English.

PS The sequence encodes STL (K41363) and is involved in the expression

of TPS (trehalose-6-phosphate synthase) catalytic activities.

XX Sequence 5981 BP; 1698 A; 1314 C; 1364 G; 1605 T; 0 other;

Query Match 16.6%; Score 27.6; J98 14; Length 5981;

Best local Similarity 49.38; Pred. No. 10;

Matches 69; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

UY 18 ccaagcgaatgaattctgaatttctctttatccatleguetttaactctatgacgaattcg 77

Db 1952 cccgcccctgacatttcaatataagtgatattggaattacttgactcaaatggttaactc 2011

UY 78 gttcagatgctccatcagctctcgtcatuaggaatcgaattccggaagtcttgattga 137

Db 2012 ggtcgaagagcctcgcgcctccacaaaggaatagaaagagcggaggtccggcgaac 2071

UY 138 taagcattagcgaatgaatt 157

Db 2072 gactatgattcgaattact 2091

Search completed: April 11, 2001, 19:50:18  
Job time: 19011 sec



















1. The first part of the paper is devoted to the study of the properties of the function  $f(x)$  defined by the equation

$\mathcal{M} = \{ \mathcal{M}_1, \mathcal{M}_2, \dots, \mathcal{M}_n \}$ 
 $\mathcal{M}_i = \{ \mathcal{M}_{i1}, \mathcal{M}_{i2}, \dots, \mathcal{M}_{in} \}$ 
 $\mathcal{M}_{ij} = \{ \mathcal{M}_{ij1}, \mathcal{M}_{ij2}, \dots, \mathcal{M}_{ijn} \}$ 
 $\mathcal{M}_{ijn} = \{ \mathcal{M}_{ijn1}, \mathcal{M}_{ijn2}, \dots, \mathcal{M}_{ijnn} \}$

Run on:	April 11, 2001, 19:00:00 - Search time 261.61 seconds (without alignments)	2.08, 870 Million updates/sec
Run on:	April 11, 2001, 19:00:00 - Search time 261.61 seconds (without alignments)	2.08, 870 Million updates/sec

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The number of transformed cells was determined by the number of colonies obtained on the selective medium. The results are the mean of three independent experiments. Error bars represent standard deviation.

[illegible][illegible]

Received 10/28/81

total number of hits set equal to zero (all other sets).

06/07/94

[illegible]

Maximal	Maternal	Infant
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80	80	80
70	70	70
60	60	60
50	50	50
40	40	40
30	30	30
20	20	20
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0	0	0

[illegible]

1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 26

$$\star := \{V(\cdot) \in \mathcal{K}_c^{\text{loc}} \mid V N_{\varepsilon} = 0 \text{ on } \partial B_1(0), \forall \varepsilon > 0\}$$

**\* NAL-88-016 \***

[illegible]

1.  $\mathcal{L}(\mathcal{A}) = \mathcal{L}(\mathcal{B})$  if and only if  $\mathcal{A} \equiv \mathcal{B}$ .

[illegible]

1.  $\mathcal{A} = \{A_1, A_2, \dots, A_n\}$  is a family of  $n$  sets.

the 1990s, the number of people in the world who are illiterate has increased from 1.2 billion to 1.5 billion. The number of illiterate people in the world is expected to reach 1.7 billion by the year 2015. The number of illiterate people in the world is expected to reach 1.7 billion by the year 2015.

$$N_{\mathcal{C}} = \frac{1}{2} \left( \frac{1}{\sqrt{2}} \begin{bmatrix} 1 & 1 \\ 1 & -1 \end{bmatrix} \otimes \frac{1}{\sqrt{2}} \begin{bmatrix} 1 & 1 \\ 1 & -1 \end{bmatrix} \right)$$
[illegible]

Prod. No. is the number of results produced by chlorine for

and is derived by analysis of the total scattering

## SUMMARY

[illegible]

What is the value of  $\frac{1}{2} \log 2$ ?

1	20	100	1000
2	40	200	2000
3	60	300	3000
4	80	400	4000
5	100	500	5000
6	120	600	6000
7	140	700	7000
8	160	800	8000
9	180	900	9000
10	200	1000	10000

Case	Initial condition	Final condition	Final condition
1	$\phi = 0$	$\phi = 0$	$\phi = 0$
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71	$\phi = 0$	$\phi = 0$	$\phi = 0$

$\alpha$	$\beta$	$\gamma$	$\delta$	$\epsilon$	$\zeta$	$\eta$	$\theta$	$\iota$	$\kappa$	$\lambda$	$\mu$	$\nu$	$\xi$	$\omicron$	$\pi$	$\rho$	$\sigma$	$\tau$	$\upsilon$	$\phi$	$\chi$	$\psi$	$\omega$
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

$\{0, \pm 1\}$

$\alpha$	$\beta$	$\gamma$	$\delta$	$\epsilon$	$\zeta$	$\eta$	$\theta$	$\iota$	$\kappa$	$\lambda$	$\mu$	$\nu$	$\xi$	$\omicron$	$\pi$	$\rho$	$\sigma$	$\tau$	$\upsilon$	$\phi$	$\chi$	$\psi$	$\omega$
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

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us-09-490-609b-465.rge

Thu Apr 12 10:22:33 2001

chromosome 9 containing a portion of the tyrosine kinase gene  
and tyrosine kinase  
2 (bases 1 to 216294)  
Rosen, L., Trask, R., Boyson, C., Qin, S., Wand, K., Alcorn, M. E. and  
Hood, L. (1997) Submission  
Submitted (Oct 1997) Department of Molecular Protein Biology, Box  
357340 University of Washington, Seattle, Washington 98195, USA  
Sequence: The tyrosine kinase gene (216294) was sequenced from  
cDNA clones obtained from a human fetal brain cDNA library. The  
sequence was identical with the published sequence (GenBank accession  
number U00001.1) except for a single nucleotide change (G to A) at  
position 11024 (GAG to GAA) which codes for Glu to Glu.

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AUTHORS

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(calpain 1 heavy chain) reveals a multidomain protein with  
internal repeats  
6511-46 (2), 201-212 (1986)  
8625066

A cDNA for the protein-tyrosine kinase substrate, p36 (calpain 1  
heavy chain) was cloned and sequenced. The sequence predicts a 339  
amino acid protein (molecular weight 44.9 kDa). The composition  
indicates that p36 is rich in charged amino acids (32.2 %). The  
sequence homology between p36 and the phosphotyrosine A-2 inhibitor,  
lipocortin 1, are found to be about 50 %. This suggests that both are  
functionally related. The function of p36 and its kinase are  
discussed.

location/qualifiers

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Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) ( United States ) 1996, 7/1 (27-36)  
CODEN: HANHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

...heavy and K light chains. The immunological specificity of the recombinant antibody, was the same as that of hMAb AE6F4 by immunoblotting analysis to the \*14\*-3\*-3\* protein, the putative antigen of hMAb AE6F4, and by immunohistochemical and immunocytological analyses using tissue sections and sputa of lung cancer patients. The transinfected BHK...

\*Lung \*cancer\*--diagnosis\*--di; \*sputum cytodiagnosis

15/3,K/7 (Item 5 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

06433780 EMBASE No: 1996097941

**Immunocytochemical detection of lung cancer cells with monoclonal antibodies to \*14\*-3\*-3\* proteins**

Setoguchi Y.; Kato M.; Shoji M.; Honjo T.; Kamei M.; Sugitani M.; Sato S.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakamishi K.; Yasumoto K.; Nagashima A.; Nakashiki H.; Suzuki T.; Imai T.; Shirahata S.; Nomoto K. Morigata Inst. of Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-ku, Yokohama 230 Japan

Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) ( United States ) 1995, 6/4 (137-144)  
CODEN: HANHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

**Immunocytochemical detection of lung cancer cells with monoclonal antibodies to \*14\*-3\*-3\* proteins**

Murine monoclonal antibodies were raised against \*14\*-3\*-3\* proteins, the antigen of human monoclonal antibody AE6F4 which had been shown potentially useful for the immunohistochemical diagnosis of lung cancer via sputum cytology. Enzyme-linked immunosorbent assays of the murine anti-\*14\*-3\*-3\* monoclonal antibodies with isolated bovine brain \*14\*-3\*-3\* isoforms showed that the antibodies were classified into four different profiles of isoform reactivity. The comparison of \*14\*-3\*-3\* isoform and lung cancer tissue on the reactivity with murine monoclonal antibodies indicated that beta isoform can be responsible for cancer recognition, whereas human monoclonal...

...was obtained. Since murine monoclonal antibodies with different isoform specificities could immunostain lung cancer cells in sputum successfully, the combination use of murine monoclonal anti-\*14\*-3\*-3\* antibodies with human monoclonal antibody AE6F4 is potentially useful for facilitating the sputum cytodiagnosis of lung cancer.

MEDICAL DESCRIPTORS:

\*Lung \*cancer\*--diagnosis\*--di

15/3,K/8 (Item 6 from file: 73)

DIALOG(R) File 73:EMBASE  
(c) 2001 Elsevier Science B.V. All rts. reserv.

06062667 EMBASE No: 1995093110

**The \*14\*-3\*-3\* protein as the antigen for lung cancer-associated human monoclonal antibody AE6F4**

Shoji M.; Kawamoto S.; Setoguchi Y.; Mochizuki K.; Honjo T.; Kato M.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakamishi K.; Yasumoto K.; Nagashima A.; Nakashiki H.; Suzuki T.; Imai T.; Nomoto K.; Murakami H. Morigata Inst Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-ku,



... Breast \*Neoplasms\*--DI; Carcinoma--DI; Neoplasms  
Metastasis

15/3,K/13 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

134362295 CA: 134(26)362295z PATENT

Endogenous gene expression assay

INVENTOR(AUTHOR): Letters, Henrik; Jorgensen, Marianne; Skakkebaek, Niels

Erik

LOCATION: Den.

ASSIGNEE: Rigshospitalet

PATENT: PCT International; WO 0134834 A2 DATE: 20010517

APPLICATION: WO 2000DK628 (20001110) \*DK 991626 (19991111)

PAGES: 76 pp. CODEN: FIXXID LANGUAGE: English CLASS: C12Q-001/68A

DESIGNATED COUNTRIES: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FR, GB, GD, GE, GM, GR, HU, ID, IL, IN, IS, JP, KE, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NZ, NO, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, FY, KG, KZ, MD, RU, TJ, TM DESIGNATED REGIONAL: GM, KE

; LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

15/3,K/14 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

134339179 CA: 134(24)339179f PATENT

Nucleic acids and proteins associated with cancer as antitumor targets

INVENTOR(AUTHOR): Burmer, Glenna C.; Brown, Joseph F.; Pritchard, David

LOCATION: USA

ASSIGNEE: Lifespan Biosciences, Inc.

PATENT: PCT International; WO 0130964 A2 DATE: 20010503

APPLICATION: WO 2000US29126 (20001020) \*US PVI61232 (19991022)

PAGES: 98 pp. CODEN: FIXXID LANGUAGE: English CLASS: C12N-000/

DESIGNATED COUNTRIES: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FR, GB, GD, GE, GM, GR, HU, ID, IL, IN, IS, JP, KE, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NZ, NO, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, VZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM DESIGNATED REGIONAL: GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

15/3,K/15 (Item 3 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(C) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

134235337 CA: 134(17)235337g JOURNAL

Proteomic analysis reveals that 14-3-3.sigma. is down-regulated in human breast cancer cells

AUTHOR(S): Vercoutter-Edouart, Anne-Sophie; Lemoine, Jerome; Le Bourhis, Xuefen; Louis, Hornez; Bolly, Benoit; Nurocombe, Victor; Revillion, Françoise; Peyrat, Jean-Philippe; Hondermarck, Hubert

LOCATION: Equipe Facteurs de Croissance, Laboratoire de Biologie du Développement, UPRES-EA, 1033, Villeneuve d'Ascq, Fr.

JOURNAL: Cancer Res. DATE: 2001 VOLUME: 61 NUMBER: 1 PAGES: 76-80

CODEN: CNREAS ISSN: 0008-5472 LANGUAGE: English PUBLISHER: American Association for Cancer Research



Chemical Name: \*14\*-3\*-3\* protein; Biological Markers; Proteins

15/3,K/10 (Item 2 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

10599731 20270713 PMID: 10810416

Usefulness of urinary nuclear matrix protein 22 (NMP22) as a marker for transitional cell carcinoma of the bladder.

Mendez V; Filieila X; Alcover JA; Molina R; Mallafre JM; Ballesta AM; Talbot-Wright R

Department of Urology, Elche University General Hospital, Miguel Hernandez University, Elche, Spain.

Anticancer research (GREECE) Mar-Apr 2000, 20 (2B) p1169-72, ISSN 0250-7005 Journal Code: 59L

Document type: Journal Article

Record type: Completed

... was 37.8% (17 out of 45), whereas that in post-treatment cases and benign diseases was 30.8% (8 out of 26) compared to \*14\*.3\* (\*3\* out of 21) for healthy volunteers. This cut-off value provided a sensitivity of 37.8% and a specificity of 80.9%. In the bladder...

Descriptors: Bladder \*Neoplasms\*--DI; \*Carcinoma, Transitional Cell\*--diagnosis--DI; \*Nuclear Proteins--urine--UR; \*Tumor Markers, Biological--urine--UR

15/3,K/11 (Item 3 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

03879151 84230536 PMID: 6547317

A word of caution in the use of neuron-specific enolase expression in tumor diagnosis.

Iranoff G; Bigner DD

Archives of pathology & laboratory medicine (UNITED STATES) Jul 1984, 108 (7) p535, ISSN 0003-9985 Journal Code: 79Z

Contract/Grant No.: 1 P01 CA32672, CA, NCI; 1 P01 NS/CA 20023-01, NS, NINDS; CA11898-13, CA, NCI

Document type: Editorial

Record type: Completed

Descriptors: \*Neoplasms\*--DI; \*Nerve Tissue Proteins --diagnostic use--DU Chemical Name: \*14\*-3\*-3\* protein; Nerve Tissue Proteins; Phosphorylase Hydrolase

15/3,K/12 (Item 4 from file: 155)

DIALOG(R) File 155: MEDLINE(R)

03757657 81029447 PMID: 6775160

Serum UDP-galactosyl transferase as a potential biomarker for breast carcinoma.

Faone JF; Waalkes TP; Baker RR; Shaper JH

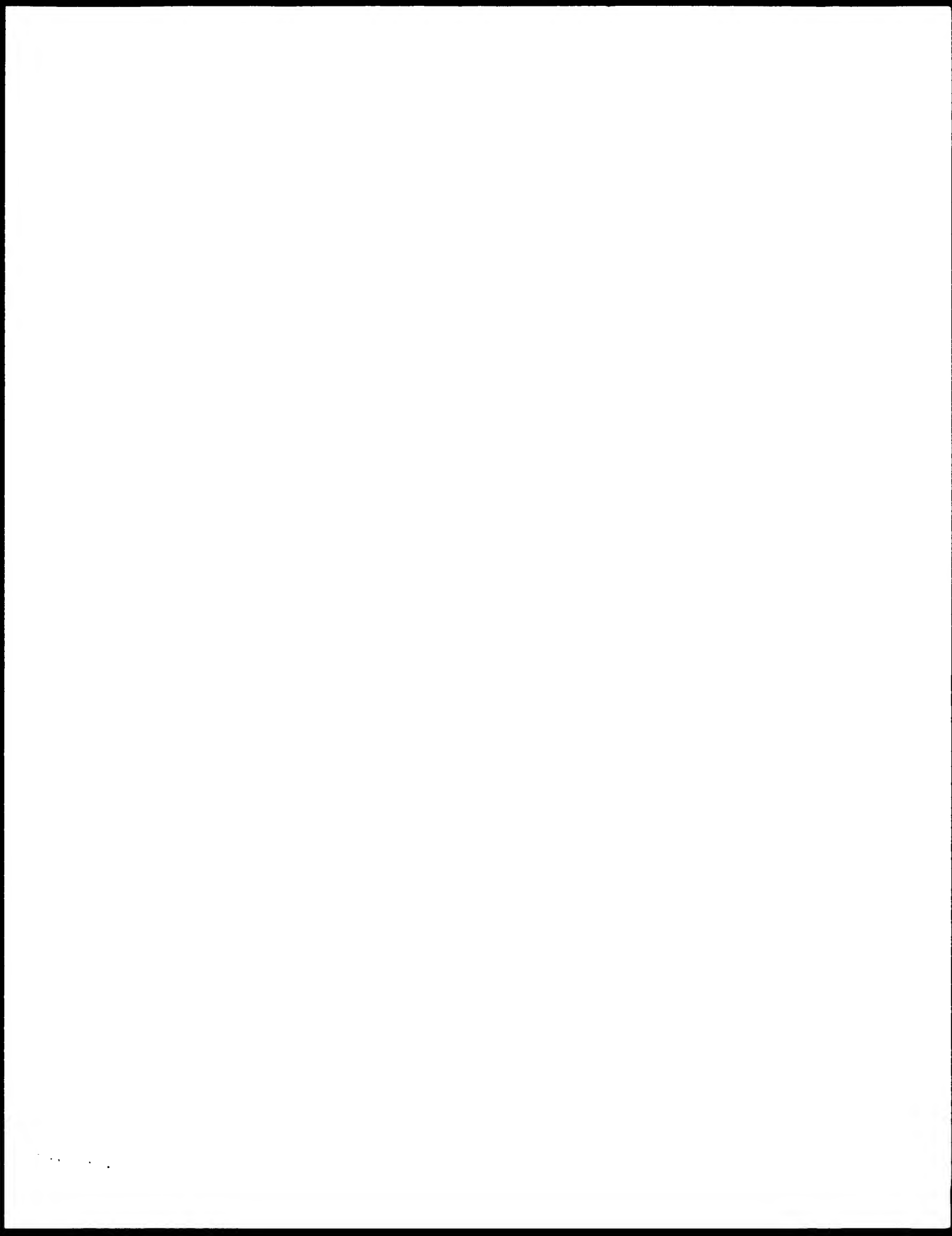
Journal of surgical oncology (UNITED STATES) 1980, 15 (1) p59-66, ISSN 0022-4790 Journal Code: K79

Contract/Grant No.: CA06973-16, CA, NCI

Document type: Journal Article

Record type: Completed

... I, II, and III, respectively). Furthermore, when serum GT levels were correlated with the preoperative clinical stage of breast cancer, significant elevations were found in \*14\*.3\* (\*3\*/21) of stage I, 66.7% (8/12) of stage II, 78.6% (11/14) of stage III, and 96.5% (28/29) of stage



Yokohama 230 Japan  
Human Antibodies and Hybridomas ( HUM. ANTIBODIES HYBRIDOMAS ) ( United States ) 1994, 5/3-4 (123-130)  
CODEN: HAHNHE ISSN: 0956-960X  
DOCUMENT TYPE: Journal; Article  
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

**The \*14\*-3\*-3\* protein as the antigen for lung cancer-associated human monoclonal antibody AE6F4**

..AE6F4-derivatized Sepharose 4B column. This 31-kDa protein was identified by the amino acid sequence analysis of the CN Br-cleared fragment as the \*14\*-3\*-3\* family of proteins, the members of which are known to play important physiological roles such as in the regulation of neurotransmitter levels and intracellular signal transduction. The purified \*14\*-3\*-3\* protein from bovine brain showed a comparable M Ab-reacting activity to that of the 31-kDa protein from A549 cells in the enzyme-linked immunosorbent assay (ELISA). The significant reactivity of bovine \*14\*-3\*-3\* protein by MAb AE6F4, shown by the cross inhibition of antibody binding to the coated 31-kDa antigen in ELISA as well as by the inhibition of immunostaining with lung cancer tissues, consistently demonstrated that the antigen(s) recognized by the M Ab was involved in the \*14\*-3\*-3\* protein family. It was found that the expression of the \*14\*-3\*-3\* protein was significantly enhanced in lung cancer tissues compared with the neighbouring normal part of the lung as examined by the immunoblotting method. These results implicated that some member(s) of the \*14\*-3\*-3\* protein family can be the tumor marker(s), providing a rational basis for the immunocytological diagnosis of lung cancer with this human M Ab. MEDICAL DESCRIPTORS: \*cancer\*--\*diagnosis\*--di

15/3,K/9 (Item 1 from file: 155)  
DIALOG(R) File 155: MEDLINE(R)

10703171 20411661 PMID: 10953182

**\*14\*-3\*-3\* testing in diagnosing Creutzfeldt-Jakob disease: a prospective study in 112 patients.**

Lemstra AW; van Meegen MT; Vreijling JP; Meijerink PH; Jansen GH; Bulk S; Baas F; van Gool WA  
Department of Neurology, Academic Medical Center, University of Amsterdam, The Netherlands. a.w.lemstra@amc.uva.nl  
Neurology (UNITED STATES) Aug 22 2000, 55 (4) p514-6, ISSN 0028-3878 Journal code: N20  
Languages: ENGLISH  
Document type: Clinical Trial; Journal Article  
Record type: Completed

**\*14\*-3\*-3\* testing in diagnosing Creutzfeldt-Jakob disease: a prospective study in 112 patients.**

OBJECTIVE: To study the sensitivity and specificity of \*14\*-3\*-3\* testing in a prospective series of patients suspected of having Creutzfeldt-Jakob disease (CJD). BACKGROUND: The \*14\*-3\*-3\* protein immunassay on CSF has favorable test characteristics as a pre-mortem diagnostic tool in CJD. However, the \*14\*-3\*-3\* protein is a normal cellular protein expressed in various tissues, and its presence in CSF reflects extensive destruction of brain tissue as in CJD, but also in ischemic stroke and meningoencephalitis. METHODS: \*14\*-3\*-3\* was tested in the CSF of a prospective series of 110 consecutive patients suspected of having CJD. RESULTS: The sensitivity was 97% and the specificity was 87% in this series. False-positive results were mainly caused by stroke and meningoencephalitis. CONCLUSION: The \*14\*-3\*-3\* protein is a highly sensitive and specific marker for CJD when used in the appropriate clinical context. Descriptors: Astrocytoma--diagnosis--DI; Brain Neoplasms--\*diagnosis\*--DI; \*Creutzfeldt-Jakob Syndrome\*--diagnosis--DI; \*Lymphoma\*--diagnosis--DI; \*Proteins\*--analysis--AN





10774690 EMBASE No: 2000254937

**simplified labeling approach for synthesizing 3'-deoxy-3' - [sup 1sup 8F]thymidine ([sup 1sup 8F]FLT)**

Machulla H.; Blocher A.; Kuntzsch M.; Piert M.; Wei R.; Grierson J.R.  
H. Machulla, Sektion Radiopharmazie, PET-Zentrum, Universitätsklinikum  
Tübingen, Röntgenweg 15, 72076 Tübingen Germany

AUTHOR EMAIL: machulla@uni-tuebingen.de  
J. R. Blocher, Journal of Radioanalytical and Nuclear Chemistry ( J. RADIOANAL. NUCL.

CHEM. ) (Hungary) 2000, 243/3 (843-846)

CODEN: JRNCD ISSN: 0236-5731

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 5

...In the case of Athy (10 mg), best FLT yields were 5.38+/-1.2 (130

degrees, 30 min). Labeling of DMTHy (10 mg) gave \*14\*.3% +/- \*3\*.3 at

160 degrees within 10 minutes. Starting with an aqueous solution of 20 GBq

[sup 1sup 8F]fluoride the new method allows to produce...

MEDICAL DESCRIPTORS:

\*tumor--diagnosis--di; \*cancer\*--\*diagnosis\*--di

**15/3,K/5 (Item 3 from file: 73)**

DIALOG(R) FILE 73:EMBASE

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07016576 EMBASE No: 1997307405

**Proteome profiling of bladder squamous cell carcinomas: Identification of markers that define their degree of differentiation**

Ostergaard M.; Rasmussen H.H.; Nielsen H.V.; Vorum H.; Orntoft T.F.; Wolf  
H.; Cells J.E.  
J.R. Cells, Department of Medical Biochemistry, Danish Ctr. for Human  
Genome Res., University of Aarhus, Ole Worms Alle, DK-8000 Aarhus C

Cancer Research ( CANCER RES. ) (United States) 1997, 57/18 (4111-4117)

CODEN: CNREA ISSN: 0008-5472

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 37

...galectin 7 and, in addition, expressed keratins 13, 15, and 19, which

were not detected in the pure SCC. Involucrin, glutathione S-transferase

pi, stratifin (\*14\*-3\*-3\* delta), and the SCC antigen 1, on the other

hand, were less abundant in SCC 589-1. In comparison? less-differentiated

tumors did not express keratin 10 and were characterized by a decreased

expression of keratin 14, psoriasin, PA-FABP, galectin 7, and stratifin (

\*14\*-3\*-3\* ). Indeed, two of these lesions (553-1 and 651-1) could be

readily lined up in order of decreasing degree of differentiation based on

the...

MEDICAL DESCRIPTORS:

article; \*cancer\* diagnosis; cell differentiation; diagnostic value;

early diagnosis; human; human tissue; priority journal

**15/3,K/6 (Item 4 from file: 73)**

DIALOG(R) FILE 73:EMBASE

(c) 2001 Elsevier Science B.V. All rts. reserv.

06668352 EMBASE No: 1996333255

**Lung cancer-reacting human recombinant antibody AE6f4: Potential usefulness in the sputum cytodiagnosis**

Shoji M.; Kawamoto S.; Seki K.; Teruya K.; Setoguchi Y.; Mochizuki K.;  
Kato M.; Hashizume S.; Hanagiri T.; Yoshimatsu T.; Nakanishi K.; Yasumoto  
K.; Nagashima A.; Nakahashi H.; Suzuki T.; Imai T.; Shitahata S.; Nomoto K.  
Morioka Inst. Biological Science, 2-1-1 Shimosueyoshi, Tsurumi-Ku,  
Yokohama 230 Japan



, antibodies to \*14\*-3\*-3\* proteins. The results of the assay demonstrated 7.2 times higher \*14\*-3\*-3\* protein content in the lung cancer tissue (378 + - 200 ng ml-1) as compared with the normal lung (54 + - 35 ng ml-1). These results indicate that the \*14\*-3\*-3\* family of proteins can be an effective marker for lung \*cancer\* \*diagnosis\* such as sputum cytodiagnosis and that \*14\*-3\*-3\* proteins might be involved in the development of lung cancers.

DESCRIPTORS:

CHEMICALS & BIOCHEMICALS: \*14\*-3\*-3\* proteins...

15/3,K/2

(Item 1 from file: 34)

DIALOG(R) File 34:SciSearch(R) Cited Ref Sci  
(c) 2001 Inst for Sci Info. All rts. reserv.

08628547 Genuine Article#: 309JM No. References: 15

Title: Usefulness of urinary nuclear matrix protein 22 (NMP22) as a marker for transitional cell carcinoma of the bladder

Author(s): Menendez V (REPRINT) ; Filella X; Alcover JA; Molina R; Mallatire JM; Ballesta AM; Talbotwright R

Corporate Source: AVDA ESCANDINAVIA 63 MF7, ALICANTE 03130//SPAIN/

(REPRINT); MIGUEL HERNANDEZ UNIV, EL CHE UNIV, GEN HOSP, DEPT

UROLOG/ELCHE//SPAIN//; HOSP CLIN BARCELONA, IDIBAPS, DEPT CLIN BIOCHEM,

CANC STUDY UNIT/BARCELONA//SPAIN//; HOSP CLIN BARCELONA, DEPT UROL &

RENAL TRANSPLANTAT/BARCELONA//SPAIN/

Journal: ANTICANCER RESEARCH, 2000, V20, N2B (MAR-APR), P1169-1172

ISSN: 0250-7005 Publication date: 20000300

Publisher: INT INST ANTICANCER RESEARCH, EDITORIAL OFFICE 1ST KM

KAPANDNTIOU-KALAMOU RD KAPANDRITI, POB 22, ATHENS 19014, GREECE

Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

...Abstract: was 37.8% (17 out of 45), whereas that in post-treatment cases and benign diseases was 30.8% (8 out of 26) compared to \*14\*.3\*.3\* (\*3\* cut of 21) for healthy volunteers. This cut-off value provided a sensitivity of 37.8% and a specificity of 80.9%. In the bladder...  
...Identifiers--FLOW-CYTOMETRY; FOLLOUP-UP; \*CANCER; \*\*DIAGNOSIS; \*CYTOLOGY

15/3,K/3

(Item 1 from file: 73)

DIALOG(R) File 73:EMBASE

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11089277 EMBASE No: 2001106912

14-3-3sigma Down-modulation: A ubiquitous marker for breast cancer?

Schmeichel K.

Breast Cancer Research ( United Kingdom ) 2000,

2/5 (373-374)

CODEN: BCRRC ISSN: 1465-5411

DOCUMENT TYPE: Journal ; Note

LANGUAGE: ENGLISH

DRUG DESCRIPTORS:

\*protein \*14\* \*3\* \*3\*-endogenous compound--ec; \*sigma factor--endogenous compound--ec

MEDICAL DESCRIPTORS:

promoter region; methylation; breast carcinogenesis--etiology--et; cancer growth--etiology--et; DNA damage; gene inactivation; breast tumor--etiology

--et; gene silencing; gene control; cancer invasion; \*cancer\* \*diagnosis\*;

human; note

CAS REGISTRY NO.: 136047-16-0 (protein \*14\* \*3\* \*3\*); 9037-42-7 (DNA

methyltransferase); 2353-33-5 (5 aza 2' deoxycytidine)

15/3,K/4

(Item 2 from file: 73)

DIALOG(R) File 73:EMBASE

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(c) 2001 The Gale Group  
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(c) format only 2000 The Dialog Corporation  
File 157:Aidsline(R) 1980-2000/Dec  
(c) format only 2000 The Dialog Corporation  
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(c) 2001 BLHCIS  
File 442:AMA Journals 1982-2001/Jul B3  
(c)2001 Amer Med Assn -FARS/DARS apply  
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(c) 2001 Informania Ltd.

Set	Items	Description
S1	0	CANCER? WITH (MARKER? OR DIAGNOS?)
S2	97610	CANCER? (W) (MARKER? OR DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5	0	(S2 OR S3 OR S4) AND REGUCALCIN
S6	2	(S2 OR S3 OR S4) AND (TSC(W)22)
S7	1	FD (unique items)
S8	18	(S2 OF S3 OF S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	FD (unique items)
S10	5	(S2 OF S3 OF S4) AND RTE
S11	2	FD (unique items)
S12	2	(S2 OF S3 OF S4) AND (ANNEXIN(W)II)
S13	2	FD (unique items)
S14	43	(S2 OF S3 OF S4) AND (14(W)3(W)3)
S15	25	FD (unique items)

MAXKMIC option is not available in file(s): 41, 77, 399

15/3,K/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)  
(c) 2001 BIOSIS. All rts. reserv.

11268954 BIOSIS NO.: 199800050286

Elevated expression levels of the \*14\*-\*3\*-\*3\* family of proteins in lung

cancer tissues.

AUTHOR: Nakamishi Kozo(a); Hashizume Shuichi; Kato Masatoshi; Honjo

Tsutsumi; Setoguchi Yuko; Yasumoto Kosei

AUTHOR ADDRESS: (a) Second Dep. Surg., Sch. Med., Univ. Occup. Environ.

Health, 1-1 Iseigaoka, Yahatanishi-ku, Kitakyu Japan

JOURNAL: Human Antibodies 8 (4):p189-194 1997

ISSN: 1093-2607

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

Elevated expression levels of the \*14\*-\*3\*-\*3\* family of proteins in lung

cancer tissues.

ABSTRACT: Immunohistochemical staining of lung cancer sections with a murine

monoclonal anti-\*14\*-\*3\*-\*3\* antibody showed a sharp discrimination of

the cancer tissue from neighboring normal counterparts in 88 of 121

primary lung cancer tissue specimens of all four...

...of normal and cancerous lung tissue homogenates, each set prepared from

surgically dissected tissues of the cancer and its surrounding normal

part, were assayed for \*14\*-\*3\*-\*3\* proteins by the sandwich

enzyme-linked immunosorbent assay using two different monoclonal



File 5: Biosis Previews(R) 1969-2001/Jul W5  
 File 6: NTIS 1964-2001/Aug W3  
 File 34: Scisearch(R) Cited Ref Sci 1990-2001/Aug W1  
 File 40: Enviroline(R) 1975-2001/Jul  
 File 41: Congressional Information Service  
 File 42: Pollution Abs 1970-2001/Aug  
 File 50: CAB Abstracts 1972-2001/Jul  
 File 51: 2001 Cambridge Scientific Abstracts  
 File 65: Inside Conferences 1993-2001/Aug W1  
 File 66: 2001 CAB International  
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 File 50: 2001 Sport Information Resource Centre





proteins. They are also substrates of receptor tyrosine kinases. Overexpression of \*Annexin\* II\*, which has been reported in various carcinomas, is thought to be associated with cell proliferation, differentiation and cell-cell adhesion in the pathogenesis of carcinoma, but the functions of Annexins have not been fully elucidated. In this study, we investigated the role of \*Annexin\* II\* (p36) and its relationship with c-erbB-2 overexpression in gastric carcinoma. We studied \*Annexin\* II\* expression using Western blot analysis in 8 human gastric carcinoma cell lines and expression of \*Annexin\* II\* and c-erbB-2 using immunohistochemistry in 153 primary gastric carcinomas. Western blot revealed that \*Annexin\* II\* was expressed in 8 human gastric carcinoma cell lines. It was more strongly expressed in the cell membrane than in the cytoplasm of tumor cells in primary gastric carcinoma tissues. Thirty-three percent of all cases were immunopositive for \*Annexin\* II\*, overexpression of which was more frequent in differentiated type (p = 0.0009), lymph node, metastasis (p = 0.0147) and venous invasion (p = 0.0092). \*Annexin\* II\* and c-erbB-2 overexpression were significantly correlated (p = 0.0002) and patients with \*Annexin\* II\* had poorer prognoses (p = 0.0066). Multivariate analysis showed that immunopositivity of both \*Annexin\* II\* and c-erbB-2 was an independent and poor prognostic factor (p = 0.0037). In conclusion, \*Annexin\* II\* was overexpressed in advanced gastric carcinomas and it could contribute to the progression of gastric carcinoma.

Descriptors: \*Annexin\* II\*-blosynthesis--BI; \*Stomach Neoplasms --metabolism--ME; \*Annexin\* II\*-physiology--PH; Prognosis; Receptor, erbB-2--blosynthesis--BI; \*Stomach Neoplasms\*--\*diagnosis\*--DI; \*Stomach Neoplasms\*--pathology--PA; Tumor Cells, Cultured

Chemical Name: \*Annexin\* II\*; Receptor, erbB-2

13/3,K/2 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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129273909 CA: 129(21)273909 JOURNAL  
Identification of genes expressed differentially by LNCaP or PC-3 prostate cancer cell lines

AUTHOR(S): Yang, Mitheng; Ioda, Massimo; Sytkowski, Arthur J.  
LOCATION: Laboratory for Cell and Molecular Biology, Division of Hematology and Oncology, Department of Medicine, Harvard Medical School, Boston, MA, 02215, USA

JOURNAL: Cancer Res. DATE: 1998 VOLUME: 58 NUMBER: 16 PAGES:

3732-3735 CODEN: CNREA8 ISSN: 0008-5472 LANGUAGE: English PUBLISHER:

2s (s2 or s3 or s4) and ((14(w)3(w)3)

>>>Unmatched parentheses

2s (s2 or s3 or s4) and (14(w)3(w)3)

Processing

Processing 10 of 44 files ...

Processing

Processing 20 of 44 files ...

Processing

Processing 30 of 44 files ...

Processing

Completed processing all files

97610 S2

347300 S3

890 S4

3426620 14

17777275 3

17777275 3

6488 14(W)3(W)3

S14 43 (S2 OR S3 OR S4) AND (14(W)3(W)3)

2nd

...completed examining records

S15 25 RD (unique items)

show files;ds;t/3,k/all



Sot	Items	Description
S1	0	CANCER? WITH (MARKER? OR DIAGNOS?)
S2	97610	CANCER? (W) (MARKER? OR DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4	890	CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5	0	(S? OR S3 OR S4) AND REGUCALCIN
S6	2	(S? OR S3 OR S4) AND (TSC(W)22)
S7	1	RD (unique items)
S8	18	(S? OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)
S9	17	RD (unique items)
S10	5	(S? OR S3 OR S4) AND BTF
S11	2	RD (unique items)
S12	2	(S? OR S3 OR S4) AND (ANNEXIN(W)II)
S13	2	RD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

13/3,K/1  
(Item 1 from file: 155)  
DIALOG(R)File 155:MEDLINE(R)

11488500 21290242 PMID: 11396210

**\*Annexin\* II\* overexpression is correlated with poor prognosis in human gastric carcinoma.**

Emoto K; Sawada H; Yamada Y; Fujimoto H; Takahama Y; Ueno M; Takayama T; Uchida H; Kamada K; Naito A; Hirao S; Nakajima Y  
First Department of Surgery, Nara Medical University, 840 Shijou-cho, Kashihara, Nara 634-8522, Japan.  
Anticancer research (Greece) Mar-Apr 2001, 21 (2B) p1339-45, ISSN 0250-7005 Journal Code: 59L  
Languages: ENGLISH  
Document type: Journal Article  
Record type: Completed

**\*Annexin\* II\* overexpression is correlated with poor prognosis in human gastric carcinoma.**

Annexins belong to a family of the calcium-dependent phospholipid binding



97610 S2  
347300 S3  
890 S4  
18158 ANNEXIN  
3840376 II  
2250 ANNEXIN(W)II  
S12 2 (S2 OR S3 OR S4) AND (ANNEXIN(W)II)

2nd  
...completed examining records  
S13 2 PD (unique items)  
show files;ds;t/3,h/all

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- File 266: FEDRIP 2001/Jul



The International Space Station (ISS) will support several facilities dedicated to scientific research. One such facility, the Biotechnology Facility (\*BTF\*), is sponsored by the Microgravity Sciences and Applications Division (MSAD) and developed at NASA's Johnson Space Center. The \*BTF\* is scheduled for delivery to the ISS via Space Shuttle in April 2005. The purpose of the \*BTF\* is to provide: (1) the support structure and integration capabilities for the individual modules in which biotechnology experiments will be performed, (2) the capability for...

... advances in the understanding of basic and applied biotechnology. Results from planned investigations can be used in applications ranging from rational drug design and testing, \*cancer\* \*diagnosis\* and treatments and tissue engineering leading to replacement tissues.

11/3/K/2 (Item 1 from file: 73)

LIALOG(P) FILE 73:EMBASE

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10845696 EMBASE No: 2000326389

**Evaluation of two new urinary tumor markers: Bladder tumor fibronectin and cytokeratin 18 for the diagnosis of bladder cancer**

Sanchez-Carbayo M.; Urrutia M.; Gonzalez de Buitrage J.M.; Navajo J.A. M. Sanchez-Carbayo, Laboratorio de Marcadores Tumores, Servicio de Bioquimica, Hospital Universitario de Salamanca, c/Paseo de San Vicente s/n, 37007 Salamanca Spain  
CLINICAL Cancer Research ( CLIN. CANCER RES. ) (United States) 2000, 6/9

CODEN: CCREF ISSN: 1078-0432

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 53

Our objectives were to evaluate the diagnostic value of two new urinary tumor markers, cytokeratin 18 (CK18) and bladder tumor fibronectin (\*BTF\*), for the detection and monitoring of bladder cancer. The study comprised 931 urine samples belonging to 402 subjects: 112 individuals under suspicion for a primary...

...urological diseases (group 4); and 32 healthy subjects (group 5). Voided urine samples were collected before cystoscopies, between them and before intravesical instillations. CK18 and \*BTF\* tests were measured by chemiluminescent immunoassays. Optimal receiver operating characteristic cutoffs of 7.4 mug/L for CK18 and 52.8 mug/liter for \*BTF\* rendered overall sensitivities of 66.2% for CK18 and 80.0% for \*BTF\* at specificities of 89.4 and 74.7%, respectively. Urinary cytology provided a sensitivity of 29.2% at a specificity of 99.1%. Sensitivities were 80.8, 74.2, and 82.3% for \*BTF\* and 71.1, 77.4, and 64.7% for CK18 for groups 1 to 3, respectively. False positive rates were higher for \*BTF\* in all groups of patients. Elevated urinary tumor markers during the monitoring of patients with bladder cancer could detect recurrence sooner than scheduled cystoscopies. Persistence of negative markers was greatly indicative of free of disease status in follow-up. CK18 and \*BTF\* in urine may eventually prove to be of benefit for specific patients with bladder carcinoma given its higher sensitivity compared with cytology. In selected patients, namely those with persistent negative urinary CK18 and \*BTF\*, the number of cystoscopies could be reduced.

MEDICAL DESCRIPTORS:

\*bladder \*cancer\*--\*diagnosis\*--di

\*cancer\* \*diagnosis\* \*diagnostic value\* \*cystoscopy\* \*chemoluminescence\*

immunoassay; receiver operating characteristic; urine cytology; diagnostic accuracy; cancer recurrence; human; male; female; major clinical study;

controlled study; human cell; aged...  
75 (s2 or s3 or s4) and (annexin(w)ii)





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S5 0 (S2 OR S3 OR S4) AND REGUCALCIN

S6 2 (S2 OR S3 OR S4) AND (TSC(W)22)

S7 1 RD (unique items)

S8 18 (S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)

S9 17 RD (unique items)

S10 5 (S2 OR S3 OR S4) AND BTF

S11 2 RD (unique items)

>>>KWIC option is not available in file(s): 41, 77, 399

11/3,K/1  
(Item 1 from file: 6)  
DIALOG(R)File 6:NTIS

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2186676 NTIS Accession Number: N20000112941/XAB

**Biotechnology Facility: An ISS Microgravity Research Facility**

Gonda, S. R. ; Tsao, Y. M.

National Aeronautics and Space Administration, Houston, TX. Lyndon B. Johnson Space Center.

Corp. Source Codes: 019042004; ND185000  
Report No.: AIAA PAPER 2000-0430

2000 9p

Languages: English

Journal Announcement: USGRLR0105; STAR3907

Presented at Aerospace Sciences 38th Reno, NV 10-13 Jan. 2000. American

Inst. of Aeronautics and Astronautics, Reston, VA.

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DESCRIPORS: rat cytosol low abundance \*epoxide\*-hydrolyase\*, gene cloning, polymerase chain reaction, pot. \*cancer\* \*diagnosis\* enzyme EC-3.3.2.2

tumor (Vol.12, No.21)  
 ?s (s2 or s3 or s4) and btf

97610 S2  
 347300 S3  
 890 S4  
 566 BTF  
 S10 5 (s2 OR S3 OR S4) AND BTF

...completed examining records

S11 2 RD (unique items)

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9/3/K/15 (Item 2 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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100083582 CA: 100(11) 83582Z JOURNAL

**Epoxide hydrolase: a marker for experimental hepatocarcinogenesis**

AUTHOR(S): Griffin, Martin J.; Gengozian, Nazareth  
LOCATION: Cancer Res. Program, Oklahoma Med. Res. Found., Oklahoma City,  
OK, 73104, USA

JOURNAL: Ann. Clin. Lab. Sci. DATE: 1984 VOLUME: 14 NUMBER: 1 PAGES:  
27-31 CODEN: ACLSCP ISSN: 0091-7370 LANGUAGE: English

9/3/K/16 (Item 1 from file: 266)

DIALOG(R) File 266:FEDRIP

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00307010

IDENTIFYING NO.: 5R01S05116-10 AGENCY CODE: CRISP

**BIOLOGICAL MARKERS OF AFLATOXIN EXPOSURE**

PRINCIPAL INVESTIGATOR: SANTELLA, REGINA M

ADDRESS: COLUMBIA UNIVERSITY 701 W 168TH ST NEW YORK, NY 10032

PERFORMING ORG.: COLUMBIA UNIVERSITY HEALTH SCIENCES, NEW YORK

SPONSORING ORG.: NATIONAL INSTITUTE OF ENVIRONMENTAL HEALTH SCIENCES

FY : 2001

...SUMMARY: of carcinogens are partly responsible for inter-individual differences in AFB1 adduct levels, by determination of genotype for glutathione S-transferase M1 and T1, and \*epoxide\*hydrolase\*. Since genotyping methods are currently unavailable to examine the role of polymorphisms in cytochrome P450 3A4 and 1A2, a quantitative immunohistochemical technique for phenotyping will...  
DESCRIPTORS: biomarker; blood chemistry; urinalysis; genotype; Taiwan; human subject; \*epoxide\*hydrolase\*; immunocytochemistry; western blotting; hepatitis B antigen; environment related neoplasm/cancer; nutrition aspect of cancer; neoplasm/\*cancer\*diagnosis\*; hepatocellular carcinoma; cancer risk; nutrition related tag; toxicant interaction; Asian; aflatoxin; toxin metabolism; glutathione transferase; DNA damage; enzyme activity; oxidative stress; smoking; clinical research

9/3/K/17

(Item 1 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs

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0154125 DBA Accession No.: 93-12177

**The use of the PCR technique in cloning low abundant genes: isolation of a cytosolic \*epoxide\*hydrolase\* cDNA- enzyme isolation, purification and gene cloning by the polymerase chain reaction; potential \*cancer\*diagnosis\* (conference paper)**

AUTHOR: Knehr M; Arand M; Hagen M; Zeller H D; Thomas H; Gsch F

CORPORATE SOURCE: Institute of Toxicology, University of Mainz, Obere

Zahlbacherstr. 67, D-6500 Mainz, Germany.

JOURNAL: Eur. Biotechnol. Today (217-22) 1992

CODEN: 9999S

LANGUAGE: English

**The use of the PCR technique in cloning low abundant genes: isolation of a cytosolic \*epoxide\*hydrolase\* cDNA- enzyme isolation, purification and gene cloning by the polymerase chain reaction; potential \*cancer\*diagnosis\* (conference paper)**

ABSTRACT: Cytosolic \*epoxide\*hydrolase\* (CEH, EC-3.3.2.2) was isolated and purified from a tiadenol-induced male rat cytosol and peptide fragments were generated by endoprotease Glu...

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RESPIRATORY TRACT DISEASES--Physiopathology--PF; MOUTH DISEASES--Pathology  
--PA; TOOTH DISEASES--Pathology--PA; SUBSTANCE-RELATED DISORDERS; POISONING  
; ANIMALS, LABORATORY; DIAGNOSIS; \*NEOPLASMS\*--DI; NEOPLASMS  
--Pathology--PA; NEOPLASMS--Metabolism--ME; MORBIDITY; NEOPLASMS; HOMINIDAE

9/3,K/12 (Item 3 from file: 156)

DIALOG(R) File 156:Toxline(R)

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03071639 Subfile: BIOSIS-91-13126

Cytochrome P-450 isozyme pattern is related to individual susceptibility to diethylnitrosamine-induced liver cancer in rats.

AITIO A; AITIO M-L; CAMUS A-M; CARDIS E; BARTSCH H

Lab. Biochem., Inst. Occup. Health, Arinatie 3, 00370 Helsinki, Finl.

Source: JPN J CANCER RES; 82 (2). 1991. 146-156. Coden: JJCRC

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS.

... of the latency period of hepatocellular tumors in individual rats was negatively related to the activities of hepatic dimethylnitrosamine N-demethylase, aryl hydrocarbon hydroxylase and \*epoxide\* \*hydroxylase\* and positively related to the amount of microsomal protein. Consistent relationships between the other 10 measured parameters and the susceptibility to DEN-induced carcinogenesis were...

Descriptors/keywords: ...; AMINO ACIDS; PEPTIDES; PROTEINS; COENZYMES; ENZYMES; ENZYMES--Analysis--AN; ENZYMES--Physiology--PH; DIGESTIVE SYSTEM DISEASES--Pathology--PA; DIGESTIVE SYSTEM--Pathology--PA; POISONING; ANIMALS, LABORATORY; DIAGNOSIS; \*NEOPLASMS\*--DI; MURIDAE

9/3,K/13 (Item 4 from file: 156)

DIALOG(R) File 156:Toxline(R)

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02938869 Subfile: BIOSIS-87-24413

DETECTION OF PRENEOPLASTIC LIVER LESIONS IN THE RAT BY USE OF MONOCLONAL ANTIBODIES AGAINST MICROSOMAL \*EPOXIDE\* \*HYDROLASE\*

Source: FOURTH SYMPOSIUM OF THE DEUTSCHEN KREBSGESELLSCHAFT, SECTION OF EXPERIMENTELLE KREBSFORSCHUNG (GERMAN CANCER SOCIETY, SECTION OF EXPERIMENTAL CANCER RESEARCH), HEIDELBERG, WEST GERMANY, MARCH 18-21, 1987.

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS. RRM

DETECTION OF PRENEOPLASTIC LIVER LESIONS IN THE RAT BY USE OF MONOCLONAL ANTIBODIES AGAINST MICROSOMAL \*EPOXIDE\* \*HYDROLASE\*

Descriptors/keywords: CONGRESSES; BIOLOGY; BIOCHEMISTRY; AMINO ACIDS; PEPTIDES; PROTEINS; CARBOHYDRATES; ENZYMES--Physiology--PH; DIGESTIVE SYSTEM DISEASES--Pathology--PA; DIGESTIVE SYSTEM--Pathology--PA; DIAGNOSIS; \*NEOPLASMS\*--DI; IMMUNITY; IMMUNOCHEMISTRY--Instrumentation

9/3,K/14 (Item 1 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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104144641 CA: 104(17)144641Y PATENT

Monitoring preneoplastic antigen

INVENTOR(AUTHOR): Hammock, Bruce D.; Ota, Kenji

LOCATION: USA

ASSIGNEE: University of California, Berkeley

PATENT: United States; US 4558004 A DATE: 851210

APPLICATION: US 478962 (830325)

PAGES: 3 pp. CODEN: USXXAM LANGUAGE: English CLASS: 435004000;





they were not even asked for a blood specimen until at least several years after their initial interview, and at that... to assess association with lung cancer susceptibility. Carcinogenesis 1991;12:1533-7.

19. Heckbert SR, Weiss NS, Hornung SK, et al. Glutathione S-transferase and \*epoxide\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers. J Natl Cancer Inst 1992;84:414-22.

20...

9/3,K/10 (Item 1 from file: 156)

DIALOG(R)File 156:Toxline(R)

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03606586 Subfile: CRISP-99-ES05116-08

BIOLOGICAL MARKERS OF AFLATOXIN EXPOSURE

SANTELLA RM

COLUMBIA UNIVERSITY, 701 WEST 168TH STR, HHSC 5-506, NEW YORK, NY 10032  
Source: Crisp Data Base National Institutes of Health

Language: ENGLISH

Document Type: Research

Spon. Agency: U.S. DEPT. OF HEALTH AND HUMAN SERVICES; PUBLIC HEALTH SERVICE; NATIONAL INST. OF HEALTH, NATIONAL INSTITUTE OF ENVIRONMENTAL

HEALTH SCIENCES

Contract Number: 5R01ES05116-08

Award Type: Grant

...of carcinogens are partly responsible for inter-individual differences in AFB1 adduct levels, by determination of genotype for glutathione S-transferase M1 and T1, and \*epoxide\* \*hydrolase\*. Since genotyping methods are currently unavailable to examine the role of polymorphisms in cytochrome P450 3A4 and 1A2, a quantitative immunohistochemical technique for phenotyping will...

Descriptors/Keywords: biomarker; blood chemistry; urinalysis; genotype; Taiwan; human subject; \*epoxide\* \*hydrolase\*; immunocytochemistry; western blotting; hepatitis B antigen; environment related neoplasm/cancer; nutrition aspect of cancer; neoplasm/cancer\* \*diagnosis\*; hepatocellular carcinoma; cancer risk; nutrition related tag; toxicant interaction; Asian/Pacific Islander; aflatoxin; toxin metabolism; glutathione transferase; DNA damage; enzyme activity; oxidative stress; smoking; clinical...

9/3,K/11 (Item 2 from file: 156)

DIALOG(R)File 156:Toxline(R)

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03125275 Subfile: BIOSIS-92-29499

Glutathione S-transferase and \*epoxide\* \*hydrolase\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers.

HECKBERT SR; WEISS NS; HORNUNG SK; EATON DL; MOTULSKY AG

Dep. Epidemiol. SC-36, Univ. Washington, Seattle, Wash. 98195.

Source: J NATL CANCER INST (BETHESDA); 84 (6). 1992. 414-422. Coden:

Language: ENGLISH

BIOSIS COPYRIGHT: BIOL ABS.

Glutathione S-transferase and \*epoxide\* \*hydrolase\* activity in human leukocytes in relation to risk of lung cancer and other smoking-related cancers.

...based, case-control study to determine whether patients with cancers related to smoking had lower activity of detoxifying isoenzymes of glutathione S-transferase (GST) and \*epoxide\* \*hydrolase\* (EH) than control subjects. Enzyme activities were measured in leukocytes from 113 King County (Washington) residents diagnosed during 1987 with one of three smoking-related...

Descriptors/Keywords: ...; PA; UROLOGIC DISEASES--Physiopathology--PP;



glutathione transferase)

9/3,K/8 (Item 5 from file: 73)

DIALOG(R) File 73:EMBASE  
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05332142 EMBASE No: 1993100227

**Expression of xenobiotic metabolizing enzymes in breast cancer**

Murray G.I.; Weaver R.J.; Paterson P.J.; Ewen S.W.B.; Melvin W.T.; Burke  
Department of Pathology, University of Aberdeen, Foresterhill, Aberdeen  
AB9 2ZD United Kingdom

Journal of Pathology ( J. PATHOL. ) (United Kingdom) 1993, 169/3

CODEN: JPTLA ISSN: 0022-3417

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

...the expression of different xenobiotic metabolizing enzymes in primary operable breast cancer of no special type. The expression of two forms of cytochrome P450, microsomal \*epoxide\* \*hydroxylase\*, and three classes of glutathione S-transferase was investigated using immunohistochemistry. The tumours were characterized by consistent expression of microsomal \*epoxide\* \*hydroxylase\* and by variable expression of the two forms of cytochrome P450 and the three types of glutathione S-transferase. Cytochrome P450 1A and cytochrome P450 3A were identified in 39 and 22 per cent of tumours, respectively. In each case, immunostaining was present only in areas of invasive carcinoma. \*Epoxide\* \*hydroxylase\* was identified in 89 per cent of tumours and glutathione S-transferases p1, mu, and alpha were identified in 56, 65, and 44 per cent of tumours, respectively. Immunoreactivity for \*epoxide\* \*hydroxylase\* and glutathione S-transferases was identified in both tumours and non-neoplastic breast tissue. The presence of different xenobiotic metabolizing enzymes may have a role...

DRUG DESCRIPTIONS:  
\*cytochrome p450--endogenous compound--ec; \*epoxide\* \*hydroxylase\*  
--endogenous compound--ec; \*glutathione transferase--endogenous compound  
--ec  
MEDICAL DESCRIPTIONS:  
\*breast cancer\*--diagnosis--di  
...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* \*hydroxylase\*); 50812-37-8 ( glutathione transferase)

9/3,K/9

(Item 1 from file: 98)

DIALOG(R) File 98:General Sci Abs/Full-Text  
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04054096 H.W. WILSON RECORD NUMBER: BGSA99054096 (USE FORMAT 7 FOR FULLTEXT)

**Glutathione S-Transferase M1 genotypes and the risk of squamous carcinoma of the cervix: a population-based case-control study.**

Chen, Chu  
Madelaine, Margaret M; Weiss, Noel S  
American Journal of Epidemiology (Am J Epidemiol) v. 150 no6 (Sept. 15 1999) p. 569-72

SPECIAL FEATURES: bibl 11 ISSN: 0002-9262

LANGUAGE: English

COUNTRY OF PUBLICATION: United States

WORD COUNT: 2881

(USE FORMAT 7 FOR FULLTEXT)

TEXT:

... several limitations. First, blood samples for genotyping were not obtained on all potentially eligible study subjects. This was a particular problem for women with cervical cancer\* diagnosed\* in the 1980s, since



...lung tissues in 12 patients. The following enzymes were assayed by Western blot analysis: cytochromes P-450 (1A1/A2, 2B1/B2, 2C8-10, 2E1, 3A4); \*epoxide\* and glutathione S- transferase isoenzymes (GST-alpha, -mu, and -pi). The activity of the following enzymes or cofactor were determined by spectrophotometric or fluorometric assays...

...GST activity and GST-alpha or GST-pi. No significant difference was observed for the glucuronide and the sulfate pathways and their corresponding hydrolytic enzymes. \*Epoxide\* and \*hydroxylase\* was significantly decreased in tumors compared to nontumoral lung tissues ( $P < 0.05$ ). In conclusion, these results showed differences between non-small cell lung tumors and nontumoral tissues for cytochrome P-450 1A1/A2 and \*epoxide\* and \*hydroxylase\*. These differences between tumors and peritumoral tissues with regard to these drug-metabolizing enzymes could reflect differences occurring after malignant transformation and may play a...

DRUG DESCRIPTIONS: \*beta glucuronidase--endogenous compound--ec; cytochrome p450--endogenous compound--ec; \*epoxide\* and \*hydroxylase\*--endogenous compound--ec; \*glucuronosyltransferase--endogenous compound--ec; \*glutathione--endogenous compound--ec; \*sulfatase--endogenous compound--ec; \*sulfotransferase--endogenous compound--ec

MEDICAL DESCRIPTIONS: \*lung non small cell cancer--surgery--su; \*lung non small cell cancer--diagnosis--di; \*lung parenchyma

...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* and \*hydroxylase\*); 37329-64-9...

9/3,K/7 (item 4 from file: 73)

DIALOG(R) FILE 73:EMBASE

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05506462 EMBASE No: 1993274561

**Xenobiotic metabolizing enzyme expression in colonic neoplasia**

McKay J.A.; Murray G.I.; Weaver R.J.; Ewen S.W.B.; Melvin W.T.; Burke

M.D.

Department of Pathology, University of Aberdeen, Foresterhill, Aberdeen

AB9 2ZD United Kingdom

Gut ( GUT ) (United Kingdom) 1993, 34/9 (1234-1239)

CODEN: GUTTA ISSN: 0017-5749

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

The cytochrome P450, \*epoxide\* and \*hydroxylase\*, and glutathione S-transferase enzyme families play an important part in the metabolism of many carcinogens and anti-cancer drugs. The expression of two forms of cytochrome P450 (P450 1A and P450 3A), \*epoxide\* and \*hydroxylase\* and of the alpha, mu, and pi forms of glutathione S-transferase in normal colonic adenomas, and adenocarcinoma of the colon were studied by...

...glutathione S-transferase pi was also present in chronic inflammatory cells. Cytochrome P450 was present in only a small proportion of normal colon samples, whereas \*epoxide\* and \*hydroxylase\* and glutathione S-transferase were identified in about half, and glutathione S-transferase alpha and pi in most normal samples. By contrast all the...

...and in over half the carcinomas. These results suggest that cytochrome P450 1A and cytochrome P450 3A are more specific markers of colonic neoplasia than \*epoxide\* and \*hydroxylase\* or glutathione S-transferases alpha, mu, and pi.

DRUG DESCRIPTIONS:

\*enzyme; \*tumor marker; \*antineoplastic agent--pharmacokinetics--pk; \*cytochrome p450--endogenous compound--ec; \*epoxide\* and \*hydroxylase\*

--endogenous compound--ec; \*glutathione transferase--endogenous compound

MEDICAL DESCRIPTIONS:

\*colon cancer--diagnosis--di; \*drug metabolism; \*xenobiotic metabolism

...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* and \*hydroxylase\*); 50812-37-8 (



polymorphisms were combined into indices of predicted microsomal \*epoxide\*  
\*hydroxylase\* activity, a decreased risk was seen among African-American  
subjects with very low predicted activity OR = 0.10 (95% CI 0.01-0.83). No

...published results for Caucasians are somewhat variable, the association  
among African-Americans in these data provides some support for the  
hypothesis that genetically reduced microsomal \*epoxide\* \*hydroxylase\*  
activity may be protective against lung cancer. (C) 2000 Elsevier Science  
Ireland Ltd.  
DRUG DESCRIPTORS:  
\*epoxide\* \*hydroxylase\*--endogenous compound--ec; \*benzo[a]pyrene--drug  
toxicity--to; \*tobacco--drug toxicity--to  
MEDICAL DESCRIPTORS:  
\*smoking; \*lung \*cancer\*--diagnosis\*--di; \*lung cancer--etiology--et; \*  
cancer risk  
...CAS REGISTRY NO.: 9048-63-9 (\*epoxide\* \*hydroxylase\*); 50-32-8 (benzo[a]pyrene)

9/3,K/5 (Item 2 from file: 73)

DIALOG(R) file 73:EMBASE  
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EMBASE No: 1999126632

Genetic polymorphism of xenobiotic metabolizing enzymes among Chinese

Lung cancer patients

Persson I.; Johansson I.; Lou Y.-C.; Yue Q.-Y.; Duan L.-S.; Bertilsson L.  
; Ingelman-Sundberg M.

I. Persson, Institute of Environmental Medicine, Division of Molecular  
Toxicology, Karolinska Institutet, 171 77 Stockholm Sweden  
AUTHOR EMAIL: irene.persson@tm.ki.se

International Journal of Cancer (INT. J. CANCER) (United States) 1999

81/3 (325-329)

CODEN: IJCA 0020-7136

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 19

...cancer susceptibility. Several studies have indicated an association  
between variant alleles of the human CYP1A1, CYP2E1 and GSTM1 genes and  
lung cancer. Activity of microsomal \*epoxide\* \*hydroxylase\* (HXL) has also  
been associated with lung cancer, and 2 variant alleles causing amino acid  
substitutions have been described. We have investigated genetic  
polymorphisms of...  
MEDICAL DESCRIPTORS:  
\*lung \*cancer\*--diagnosis\*--di; \*lung cancer--epidemiology--ep; \*lung  
cancer--etiology--et; \*genetic polymorphism; \*xenobiotic metabolism; \*  
ethnic difference

9/3,K/6 (Item 3 from file: 73)

DIALOG(R) file 73:EMBASE  
(C) 2001 Elsevier Science B.V. All rts. reserv.

EMBASE No: 1993304401

Main drug- and carcinogen-metabolizing enzyme systems in human non-small  
cell lung cancer and peritumoral tissues

Toussaint C.; Albin N.; Massaad L.; Grunewald D.; Parise Jr. O.; Morizet  
J.; Gouyette A.; Chabot G.G.

Institut Gustave-Roussy, Pavillon de recherche 2, 94805 Villejuif Cedex

France

Cancer Research ( CANCER RES. ) (United States) 1993, 53/18 (4608-4612)

CODEN: CNREA ISSN: 0008-5472

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH





02079661 Genuine Article#: J2430 No. References: 55

**Title: COMPARISON OF MOUSE AND HUMAN COLON TUMORS WITH REGARD TO PHASE-I AND PHASE-II DRUG-METABOLIZING ENZYME-SYSTEMS**

Author(s): MASSAAD L; DEWAZIERS I; RIBRAG V; JANOT F; BEAUNE PH; MORIZET J; GOUETTE A; CHABOT G

Corporate Source: INST GUSTAVE ROUSSY, PHARMACOL CLIN

LAB, CNRS, URA147, INSERM, U140/F-94805 VILLEJUIF//FRANCE//; CHU NECKER

ENRATES MAIA, INSERM LAB, U75/F-75730 PARIS 15//FRANCE//

Journal: CANCER RESEARCH, 1992, V52, N23 (DEC 1), P6567-6575

ISSN: 0008-5472

Language: ENGLISH Document Type: ARTICLE (Abstract Available)

...Abstract: both tumoral and nontumoral colon tissues. The following enzymes were assayed by Western blot: cytochromes P-450 (1A1/A2, 2B1/B2, 2C, 2E1, and 3A), \*epoxide\* \*hydrolase\*, and glutathione-S-transferases (GST- $\alpha$ , - $\mu$ , and - $\pi$ ). The activities of the following enzymes or cofactors were determined by spectrophotometric or fluorometric assays: total cytochrome P-450, 1-chloro-2,4-dinitrobenzene-GST, selenium-independent glutathione peroxidase, 3,4-dichloronitrobenzene-GST, ethacrynic acid-GST, total glutathione, \*epoxide\* \*hydrolase\*, UDP-glucuronosyltransferase, beta-glucuronidase, sulfoxidase, and sulfatase. Results obtained by Western blot showed that mouse colon adenocarcinoma C38 did not express any of the probed...

...fold higher in human tumors than in peritumoral tissues, whereas they were 7-fold lower in mouse colon tumor C38, compared to normal mouse colon. \*Epoxide\* \*hydrolase\* was not expressed in either mouse colon adenocarcinoma C38 or normal mouse colon tissues, whereas it was expressed in human colon peritumoral and tumoral tissues...

...Identifiers: GLUTATHIONE-S-TRANSFERASE; HUMAN-LIVER; AROMATIC-HYDROCARBONS; MULTIDRUG RESISTANCE; HUMAN-TISSUES; RAT-LIVER; CYTOCHROME-P-450; PURIFICATION; \*CANCER\*; \*MARKER\*

9/3,K/4 (Item 1 from file: 73)

DIALOG(F) File 73:EMBASE

(c) 2001 Elsevier Science B.V. All rts. reserv.

10626265 EMBASE No: 2000092044

**Lung cancer risk in relation to genetic polymorphisms of microsomal \*epoxide\* \*hydrolase\* among African-Americans and Caucasians in Los Angeles County**

London S.T.; Smart J.; Daly A.K.

S.T. London, Epidemiology Branch, Natl. Inst. of Environ. Health Sci., PO Box 12233, Research Triangle Park, NC 27709 United States

AUTHOR EMAIL: london2@niehs.nih.gov

Lung Cancer ( LUNG CANCER ) (Ireland) 2000, 28/2 (147-155)

CODEN: LUNCAE ISSN: 0169-5002

PUBLISHER ITEM IDENTIFIER: S0169500299001300

DOCUMENT TYPE: Journal; Article

LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH

NUMBER OF REFERENCES: 15

**Lung cancer risk in relation to genetic polymorphisms of microsomal \*epoxide\* \*hydrolase\* among African-Americans and Caucasians in Los Angeles County**

...08, 95. CI 0.01-0.62). When data from both the exon 3 and exon 4



Set Items Description  
 S1 0 CANCER? WITH (MARKER? OR DIAGNOS?)  
 S2 97610 CANCER? (W) (MARKER? OR DIAGNOS?)  
 S3 347300 NEOPLAS? (W) (MARKER? OR DIAGNOS?)  
 S4 890 CARCINOGEN? (W) (MARKER? OR DIAGNOS?)  
 S5 0 (S2 OR S3 OR S4) AND REGUCALCIN  
 S6 2 (S2 OR S3 OR S4) AND (TSC(W)22)  
 S7 1 RD (unique items)  
 S8 18 (S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)  
 S9 17 RD (unique items)  
 >>>KWIC option is not available in file(s): 41, 77, 399

9/3,K/1 (Item 1 from file: 5)

DIALOG(R) File 5: Biosis Previews(R)  
 (c) 2001 BIOSIS. All rts. reserv.

05370628 BIOSIS NO.: 000032093757

**IMMUNOCHEMICAL DETERMINATION OF MICROSOMAL \*EPOXIDE\* \*HYDROLASE\***  
**PRENEOPLASTIC ANTIGEN IN EXTRAHEPATIC TISSUE**

AUTHOR: MOODY D E; LOURY D N; HAMMOCK B D  
 AUTHOR ADDRESS: CENT. FOR HUMAN TOXICOL., 38 SKAGGS HALL, UNIV. OF UTAH,  
 SALT LAKE CITY, UTAH 84112.

JOURNAL: BIOCHEM PHARMACOL 36 (4). 1987. 570-572. 1987  
 FULL JOURNAL NAME: Biochemical Pharmacology

CODEN: BOPCA  
 RECORD TYPE: citation  
 LANGUAGE: ENGLISH

**IMMUNOCHEMICAL DETERMINATION OF MICROSOMAL \*EPOXIDE\* \*HYDROLASE\***  
**PRENEOPLASTIC ANTIGEN IN EXTRAHEPATIC TISSUE**  
 DESCRIPTORS: RAT DIAGNOSIS \*NEOPLASTIC\* MARKER\* CARCINOGENESIS

9/3,K/2 (Item 1 from file: 34)

DIALOG(R) File 34: SciSearch(R) cited Ref Sci  
 (c) 2001 Inst for Sci Info. All rts. reserv.

05970832 Genuine Article#: XLI62 No. References: 49

**Title: Tumor-specific expression of cytochrome P450 CYP1B1**

Author(s): Murray GI (REPRINT); Taylor MC; McFadyen MCE; McKay JA;  
 Greenlee WF; Burke MD; Melvin WT

Corporate Source: UNIV ABERDEEN, DEPT PATHOL, FORESTERHILL/ABERDEEN AB25  
 22D//SCOTLAND/ (REPRINT); UNIV ABERDEEN, DEPT CELL & MOL BIOL/ABERDEEN  
 AB25 22D//SCOTLAND/; UNIV MASSACHUSETTS, SCH MED, DEPT MOL PHARMACOL &  
 TOXICOL/WORCESTER/MA/01555; DE MONTFORT UNIV, DEPT PHARMACEUT

JOURNAL: CANCER RESEARCH, 1997, V57, N14 (JUL 15), P3026-3031  
 ISSN: 0008-5472 Publication date: 19970715

Publisher: AMER ASSOC CANCER RESEARCH, PUBLIC LEDGER BLDG, SUITE 816, 150  
 S. INDEPENDENCE MALL W., PHILADELPHIA, PA 19106  
 Language: English Document Type: ARTICLE (ABSTRACT AVAILABLE)

...Abstract: brain, and testis, There was no detectable immunostaining for  
 CYP1B1 in normal tissues. These results provide the basis for the  
 development of novel methods of \*cancer\* diagnosis\* based on the  
 identification of CYP1B1 in tumor cells and the development of  
 anticancer drugs that are selectively activated in tumors by CYP1B1.  
 ...Identifiers--METABOLIZING ENZYME-SYSTEMS; MICROSOMAL \*EPOXIDE\*  
 \*HYDROLASE\*; AMINO-ACID SEQUENCE; ADRENAL CYTOCHROME-P450; NEOPLASTIC  
 LESIONS; GENE SUBFAMILY; BREAST-CANCER; HUMAN KIDNEY; HUMAN LIVER; RAT  
 CYP1B1

9/3,K/3 (Item 2 from file: 34)

DIALOG(R) File 34: SciSearch(R) cited Ref Sci  
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 (c) 2001 AMERICAN CHEMICAL SOCIETY  
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 (c) 2001 DECHEMA  
 File 357: Derwent Biotechnology Abs 1982-2001/Sep B1  
 (c) 2001 Derwent Publ Ltd  
 File 358: Current Biotech Abs 1983-2001/May  
 (c) 2001 DECHEMA  
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 1999 (c) Action Potential  
 File 149: TCG Healthwelfare DB(SM) 1976-2001/Jul W5  
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 (c) format only 2000 The Dialog Corporation  
 File 157: Aidsline(R) 1980-2000/Dec  
 (c) format only 2000 The Dialog Corporation  
 File 159: Cancerlit 1975-2001/Jun  
 (c) format only 2001 Dialog Corporation  
 File 164: Allied & Complementary Medicine 1984-2001/Aug  
 (c) 2001 BLHCIS  
 File 442: AMA Journals 1982-2001/Jul B3  
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 File 444: New England Journal of Med. 1985-2001/Aug W1  
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 File 467: Extramed(tm) 2000/Dec  
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. Set      Items      Description
S1         0          CANCER? WITH (MARKER? OR DIAGNOS?)
S2        97610       CANCER? (W) (MARKER? OR DIAGNOS?)
S3        347300      NEOPLAS? (W) (MARKER? OR DIAGNOS?)
S4         890        CARCINOGEN? (W) (MARKER? OR DIAGNOS?)
S5         0          (S2 OR S3 OR S4) AND REGUCALCIN
S6         2          (S2 OR S3 OR S4) AND (TSC(W)22)
S7         1          RD (unique items)
>>>KWIC option is not available in file(s): 41, 77, 399

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7/3,K/1 (item 1 from file: 155)  
DIALOG(R) File 155:MEDLINE(R)

10852046 20526087 PMID: 11072240  
Novel association of a diverse range of genes with renal cell carcinoma

as identified by differential display.  
Rae FK; Stephenson SA; Nicol DL; Clements JA  
Centre for Molecular Biotechnology, School of Life Sciences, Queensland  
University of Technology, Brisbane, Australia.  
International Journal of Cancer. Journal International du Cancer (UNITED  
STATES) Dec 1 2000; 88 (5) p726-32, ISSN 0020-7136 Journal code:  
LANGUAGES: ENGLISH  
Document type: Journal Article  
Record type: Completed

... G-protein signalling (RGS-5), Notch-3, Na,K-ATPase alpha subunit, HLA  
class II antigen, ETS-like protein, transforming growth factor  
beta-stimulated clone (\*TSC\*22\*), bladder cancer-related protein (BC10)  
and adipophilin. Semi-quantitative RT-PCR using specific primers to each of  
these genes confirmed differential expression in 67% to...  
! Blotting, Northern; Carcinoma, Renal Cell--diagnosis--DI; DNA,  
Complementary--analysis--AN; Kidney \*Neoplasms\*--\*diagnosis\*--DI; Reverse  
Transcriptase Polymerase Chain Reaction  
S2 (S2 or S3 or S4) and (epoxide(w)hydrolase)

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97610 S2
347300 S3
890 S4
94405 EPOXIDE
171611 HYDROLASE
13169 EPOXIDE(W)HYDROLASE
S8      18      (S2 OR S3 OR S4) AND (EPOXIDE(W)HYDROLASE)
2nd

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...completed examining records  
S9 17 RD (unique items)  
show files:ds/t/3,k/all

File 5: Biosis Previews(R) 1969-2001/Jul W5  
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File 6: NTIS 1964-2001/Aug W3  
Compendstr 2000 NTIS, Intl Copyright All Right

File 34: SclSearch(F) Cited Ref Sci 1990-2001/Aug W1  
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... and 50/162 (31%) HIV-'s [OR 4.1, 95% CI 2.6-6.4] and by SB in 76/222 (34%) and 19/141 (\*14%) [\*3%\*.3\*,1.8-6.1], respectively. Pap smear showed SIL in 53/316 (17%) of HIV+'s and 9/208 (4%) HIV-'s [4.5,2...  
; Adolescence; Adult; Blotting, Southern; Cervical Intraepithelial Neoplasia\*--\*Diagnosis\*--DI; Cervical Intraepithelial Neoplasia--Virology --VI; CD4 Lymphocyte Count; DNA, Viral--Analysis--AN; Ethnic Groups; Middle Age; Polymerase Chain Reaction; Risk Factors; Vaginal Smears

15/3,K/25 (Item 1 from file: 159)

DIALOG(R) File 159: Cancerlit

(c) Format only 2001 Dialog Corporation. All rts. reserv.

01481564 99195577 PMID: 10095843

**Endoscopic patterns of primary gastric MALT lymphoma.**

Aoun JF; Moukareb N; Khoury S

Division of Gastroenterology, Saint Georges Hospital, Beirut, Lebanon.  
J Med Liban; 46 (3) p131-5 1998 (LEBANON) May-Jun 1998, ISSN 0023-9852 Journal Code: J1Z

Languages: ENGLISH

Document Type: Journal Article

Record type: Completed

... treated for primary gastric MALT lymphomas, were reviewed. Four main patterns were recognized: 1/Large ulcerations (n = 6, 42.9%), 2/Polypoid lesion (n = 2, \*14%\*.3\*), \*3\*/Gastritis with small ulcerations (n = 4, 28.5%), and 4/Atypical mucosal relief (AMR): erythema, nodularity, edematous or infiltrated folds (n = 2, 14.3%). In...  
Major Descriptors: Lymphoma, Mucosa-Associated Lymphoid Tissue--diagnosis --DI; \*Stomach \*Neoplasms\*--\*diagnosis\*--DI

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sequences: Lys-Ala-Val-Thr-Glu...

... lines, human cancer tissue, human cancer cells in sputa, and IgM, but not with normal human cells. The MAbs can be used for human lung cancer \*diagnosis\* and in particular, for detection of the mRNA coding for the protein sequence. In a preferred embodiment, lymphocytes are isolated from healthy human peripheral blood...

DESCRIPTORS: \*14\*-3\*-3\* protein, phospholipase-A2 human monoclonal antibody prep., hybridoma construction, appl. lung cancer \*diagnosis\* mammalian animal cell culture tumor enzyme EC-3.1.1.4 (Vol.14, No.24)

15/3,K/23 (Item 1 from file: 149)

DIALOG(R) File 149: TGG Health&Wellness DB(SM)  
(c) 2001 The Gale Group. All rts. reserv.

01951833 SUPPLIER NUMBER: 67161662 (USE FORMAT 7 OR 9 FOR FULL TEXT)

**Proteomics: new perspectives, new biomedical opportunities. (Seminar)**

Banks, Rosamonde E; Dunn, Michael J; Hochstrasser, Denis F; Sanchez, Jean-Charles; Blackstock, Walter; Pappin, Darryl J; Selby, Peter J  
The Lancet, 356, 9243, 1749  
Nov 18, 2000

PUBLICATION FORMAT: Magazine/Journal; Refereed ISSN: 0099-5355  
LANGUAGE: English RECORD TYPE: Fulltext; Abstract TARGET AUDIENCE:

Professional

WORD COUNT: 7033 LINE COUNT: 00604

... discriminate between CJD and other types of dementia with a sensitivity of 88% and specificity of 99%. (29) Sequencing identified them as members of the \*14\*-3\*-3\* family. The value of \*14\*-3\*-3\* proteins as discriminatory markers for CJD in patients with dementia has since been confirmed in several studies, (30,31) although clinical use in CJD has... (25) Genetic markers, detected cytogenetically or by mutation detection, are also now entering clinical practice, 58 but some changes likely to be important in \*carcinogenesis\*, \*diagnosis\*, and prognosis, such as abnormal expression of proto-oncogenes, may not be associated with a detectable genetic lesion. For proteins implicated in cancer, the use... of patients with Creutzfeldt-Jakob disease. N Engl J Med 1986; 315: 279-83. (30) Zerr I, Bodemer M, Gellner O, et al. Detection of \*14\*-3\*-3\* protein in the cerebrospinal fluid supports the diagnosis of Creutzfeldt-Jakob disease. Ann Neurol 1998; 43: 32-40. (31) Beaudry P, Cohen P, Brandel JP, et al. \*14\*-3\*-3\* protein, neuron-specific enolase, and S-100 protein in cerebrospinal fluid of patients with Creutzfeldt-Jakob disease. Dementia Geriatr Cogn Dis 1999; 10: 40-46. MJ, et al. Characterization of endothelial antigens associated with transplant-associated coronary artery disease. J Heart Lung Transplant 1995; 14: S188-97. (58) Sell S. \*Cancer\* markers\* of the 1990s: comparison of the new generation of markers defined by monoclonal antibodies and oncogene probes to prototypic markers. Clin Lab Med 1990; 10...

15/3,K/24 (Item 1 from file: 157)

DIALOG(R) File 157: Aidsline(F)

(c) Format only 2000 The Dialog Corporation. All rts. reserv.

00176175 95920227

**Genital human papillomavirus (HPV) infection and squamous intraepithelial lesions (SIL) on pap smear in women at risk for HIV infection.**

Klein RS; Shah K; Cu-Uvin S; Schuman P; Solomon L; Warren D; Burk RD  
Montefiore Einstein, Bronx NY.  
Natl Conf Hum Retroviruses Relat Infect (2nd) (UNITED STATES) Jan

29-Feb 2 1995, p90,  
Languages: ENGLISH  
Document Type: MEETING ABSTRACTS

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with the phosphorylation-specific interaction between them. The protein and substrate are incubated in...

... and the level of interaction is compared to that of non-mutants and the mutated partner is diagnosed. Measurement of protein binding at TCAK1-mediated \*14\*-3\*-3\* recognition sites could be used to detect cancers. (75pp)  
DESCRIPTORS: recombinant twenty-five C-associated protein-kinase-1 prep., expression in host cell, antibody, appl. \*cancer\* \*diagnosis\* enzyme EC-2.7.1.37 protein sequence DNA sequence tumor (Vol.17, No.9)

15/3,K/21 (Item 4 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs  
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0216582 DBA Accession No.: 97-11703 PATENT

Anti-\*14\*-3\*-3\* protein mouse monoclonal antibody and a method for the  
inspection of human lung cancer - hybridoma cell culture

CORPORATE SOURCE: Japan.

PATENT ASSIGNEE: Morinaga 1997

PATENT NUMBER: JP 9187291 PATENT DATE: 970722 WPI ACCESSION NO.:

97-419404 (9739)

PRIORITY APPLIC. NO.: JP 9618031 APPLIC. DATE: 960109

LANGUAGE: JA

Anti-\*14\*-3\*-3\* protein mouse monoclonal antibody and a method for the

inspection of human lung cancer

ABSTRACT: A new mouse monoclonal antibody (MAb) recognizing \*14\*-3\*-3\* protein can be contained in a reagent for the diagnosis of human lung cancer. In an example, \*14\*-3\*-3\* protein family was purified from cattle brain and seven isoforms were separated by reverse phase HPLC. They were identified by the elution site and SDS...

...protein and fused with mouse myeloma cell line P3-X63-Ag8-UI (P3UI). The used cell (hybridoma) was cultured and screened for production of anti-\*14\*-3\*-3\* MAb by yeast-labeling immunoassay. The MAb was produced and purified. The reactivity of the MAb was tested by immunoblotting and checked by ELISA against each form of \*14\*-3\*-3\* protein. The reactivity against cancer tissue was also investigated.

DESCRIPTORS: cattle brain \*14\*-3\*-3\* protein tumor-associated antigen mouse monoclonal antibody, hybridoma, appl. human lung \*cancer\* \*diagnosis\* cell culture mammal animal (Vol.16, No.23)

15/3,K/22 (Item 5 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs  
(c) 2001 Derwent Publ Ltd. All rts. reserv.

0186928 DBA Accession No.: 95-14443 PATENT

Antibody against human lung cancer cells used for screening of human lung  
cancer- human monoclonal antibody preparation by hybridoma  
construction for use in lung \*cancer\* \*diagnosis\*

PATENT ASSIGNEE: Morinaga; New-Technol.Japan 1995

PATENT NUMBER: JP 7206900 PATENT DATE: 950808 WPI ACCESSION NO.:

95-309100 (9540)

PRIORITY APPLIC. NO.: JP 9417475 APPLIC. DATE: 940704

NATIONAL APPLIC. NO.: JP 9417475 APPLIC. DATE: 940704

LANGUAGE: JA

- human monoclonal antibody preparation by hybridoma construction for use

in lung \*cancer\* \*diagnosis\*

ABSTRACT: An antibody (Ab) is claimed, which recognises a protein, particularly \*14\*-3\*-3\* protein or cytoplasmic phospholipase-A2 (EC-3.1.1.4), and has the following protein sequence and its modified



15/3,K/19 (Item 2 from file: 357)

DIALOG(R) File 357: Derwent Biotechnology Abs (c) 2001 Derwent Publ Ltd. All rts. reserv.

0247764 DBA Accession No.: 2000-02254 PATENT

Use of \*14\*-3\*-3\* sigma polypeptides and nucleic acids for the diagnosis

or treatment of cancer- recombinant protein production via

vector-mediated gene transfer and expression in host cell for therapy

AUTHOR: Hermeking H; Gelstein B; Kinzler K W  
CORPORATE SOURCE: Baltimore, MD, USA.  
PATENT ASSIGNEE: Univ. John-Hopkins 1999

PATENT NUMBER: WO 9931240 PATENT DATE: 19990624 WPI ACCESSION NO.:

2000-022907 (2002)

PRIORITY APPLIC. NO.: US 210748 APPLIC. DATE: 19981215

NATIONAL APPLIC. NO.: WO 99US26924 APPLIC. DATE: 19991218

LANGUAGE: English

Use of \*14\*-3\*-3\* sigma polypeptides and nucleic acids for the diagnosis

or treatment of cancer

ABSTRACT: The use of \*14\*-3\*-3\* -sigma proteins and nucleic acids for

developing agents for the diagnosis, determining susceptibility to or

for treating cancers and identifying agents for treating cancers, is

new. Also claimed are: a method for suppressing the growth of a tumor

which involves administering a \*14\*-3\*-3\* -sigma 248 amino acid

protein sequence (II), which has a 1,320 bp DNA sequence (I) (both

specified) to the cells; a method for diagnosing cancer which involves

testing a tissue to determine in the tissue expresses less \*14\*-3\*-3\*

-sigma protein than normal tissue; a \*14\*-3\*-3\* -sigma reporter

construction containing a \*14\*-3\*-3\* -sigma transcription regulatory

region covalently linked in a cis configuration to a gene encoding an

assayable product; an antisense \*14\*-3\*-3\* -alpha construct; a method

for promoting cell growth via administration of the antisense

construct; a method for screening for potential antitumor agents; a

vector containing...

DESCRIPTORS: recombinant \*14\*-3\*-3\* -sigma protein prep., vector-mediated

gene transfer, expression in host cell, antisense molecule, appl.

\*cancer\* diagnosis\*, therapy, gene therapy DNA sequence protein

sequence tumor (Vol.19, No.5)

15/3,K/20

(Item 3 from file: 357)

DIALOG(R) File 357: Derwent Biotechnology Abs (c) 2001 Derwent Publ Ltd. All rts. reserv.

0222751 DBA Accession No.: 98-04348 PATENT

DNA encoding the twenty-five C-associated protein-kinase-1 (TcAK1) -

recombinant protein expression in host cell, antibody production and

application to \*cancer\* diagnosis\*

AUTHOR: Plimica-Worms H

CORPORATE SOURCE: St. Louis, MO, USA.

PATENT ASSIGNEE: Univ. Washington-St. Louis 1998

PATENT NUMBER: WO 9801756 PATENT DATE: 980115 WPI ACCESSION NO.:

98-101198 (9809)

PRIORITY APPLIC. NO.: US 677298 APPLIC. DATE: 960709

NATIONAL APPLIC. NO.: WO 97US11721 APPLIC. DATE: 970703

LANGUAGE: English

- recombinant protein expression in host cell, antibody production and

application to \*cancer\* diagnosis\*

..ABSTRACT: TcAK1 produced. An antibody specifically reactive with a

Tackl-kinase or an internal C-terminal peptide is claimed. A method is

claimed for creating a \*14\*-3\*-3\* recognition motif within a TcAK1

substrate by incubating the substrate in a recombinant transformed

cell. A method is claimed of detecting a mutation in a \*14\*-3\*-3\*

protein or a TcAK1 substrate where the mutation prevents or intereferes





15/3,K/16 (Item 4 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

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127133100 CA: 127(10)133100v PATENT

Anti-14-3-3 mouse monoclonal antibodies, diagnostic agents for human lung

cancer, and diagnostic method

INVENTOR(AUTHOR): Setoguchi, Hiroko; Kamel, Masanori; Kato, Masatoshi

LOCATION: Japan,

ASSIGNEE: Morinaga and Co., Ltd.; Research Development Corp. of Japan

19970722

APPLICATION: JP 9618031 (19960109)

PAGES: 6 pp. COIN: JPKXAF LANGUAGE: Japanese CLASS: C12P-021/08A;

G01N-033/574B; G01N-033/577B; C12N-005/10B

15/3,K/17 (Item 5 from file: 399)

DIALOG(R) File 399:CA SEARCH(R)

(c) 2001 AMERICAN CHEMICAL SOCIETY. All rts. reserv.

123225953 CA: 123(17)225953w PATENT

Antibody to phospholipase A for lung cancer diagnosis

INVENTOR(AUTHOR): Sato, Susumu; Kamel, Masanori; Hashizume, Shuichi;

Nomoto, Kikuo; Murakami, Hiroaki

LOCATION: Japan,

ASSIGNEE: Morinaga & Co.; Shingijutsu Kaishatsu Jigyodan; Nomoto Kikuo;

Murakami Hiroaki

PATENT: Japan Kokai Tokkyo Koho ; JP 95206900 A2 ; JP 07206900 DATE:

950808

APPLICATION: JP 94174775 (940704) \*JP 93304187 (931203)

PAGES: 10 pp. COIN: JPKXAF LANGUAGE: Japanese CLASS: C07K-016/30A;

A61K-039/395B; C12P-021/08B; G01N-033/53B; G01N-033/574B; G01N-033/577B;

C12N 015/02; C12P-021/08J; C12F-001/91J

15/3,K/18 (Item 1 from file: 357)

DIALOG(R) File 357:Derwent Biotechnology Abs

(c) 2001 Derwent Publ Ltd. All rts. reserv.

0254020 DBA Accession No.: 2000-08510 PATENT

New complex of a NLK1 protein and its interacting protein useful for

treating cancer, hyperproliferative disorder, neurodegenerative

disorder, cardiomyopathies, virus infections and metabolic disorders-

recombinant protein and interacting protein complex production via

vector plasmid-mediated gene transfer and expression in host cell for

\*cancer\* diagnosis\* and therapy

AUTHOR: Nandabalan K; Schultz V P; Yang M

CORPORATE SOURCE: New Haven, CT, USA.

PATENT ASSIGNEE: Curagen 2000

PATENT NUMBER: WO 00020448 PATENT DATE: 20000413 WPI ACCESSION NO.:

2000-303742 (20026)

PRIORITY APPLIC. NO.: US 167206 APPLIC. DATE: 19981006

NATIONAL APPLIC. NO.: WO 99US23314 APPLIC. DATE: 19991006

LANGUAGE: English

- recombinant protein and interacting protein complex production via vector  
plasmid-mediated gene transfer and expression in host cell for \*cancer\*

\*diagnosis\* and therapy

...ABSTRACT: (C1) of an NLK1 protein and an NLK1

protein-interacting protein (IP), where NLK1 protein-IP is selected

from TrkA, protein-phosphatase-1-alpha, \*14\*-3\*-3\*-alpha,

alpha-tropomyosin, vimentin, p0071, Int-1, IP-1, -2, -3, -4 or -5, is

new. Also claimed are: a purified complex (C2) which is...











Set	Items	Description
S1	4	TS022 (S) PAT
S2	4	RD unique items

>>>RWIT option is not available in file(s): 399

2/3,K/1 (Item 1 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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138104843 CA: 138(8)104843m JOURNAL

Differential regulation of functional gene clusters in overt coronary

artery disease in a transgenic atherosclerosis-hypertensive rat model

AUTHOR(S): Herrera, Victoria L. M.; Didishvili, Tamara; Lopez, Lyle V.;

Ruiz-Opazo, Nelson

LOCATION: Unit of Molecular Genetics, Whitaker Cardiovascular Institute,

Section of Molecular Medicine, Evans Department of Medicine, Boston

University School of Medicine, Boston, MA, USA

JOURNAL: Mol. Med. (Baltimore, MD, U. S.) (Molecular Medicine (Baltimore,

MD, United States)) DATE: 2001 VOLUME: 8 NUMBER: 7 PAGES: 367-375

COMMENT: NUMBER3 ISSN: 1076-1551 LANGUAGE: English PUBLISHER: Johns

Hopkins University Press

2/3,K/2 (Item 2 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

(c) 2002 American Chemical Society. All rts. reserv.

131238831 CA: 131(18)238831v PATENT

Protein and cDNA sequences encoding a human TSC-22 homolog

INVENTOR(AUTHOR): Hillman, Jennifer L.; Lal, Preethi; Shah, Furai

LOCATION: USA

ASSIGNEE: Incyte Pharmaceuticals, Inc.

PATENT: United States; US 5958690 A DATE: 19990928

APPLICATION: US 5958337 (19970708)

PAGES: 35 pp. COMMENT: USXXAM LANGUAGE: English CLASS: 43506000;

C12:001/68A; C12F:021/02B; C12N:001/21B; C12N:154/12B

2/3,K/3 (Item 3 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

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126260113 CA: 126(20)260113f JOURNAL

Molecular cloning and characterization of a transcription factor for the

C-type natriuretic peptide gene promoter

AUTHOR(S): Ohta, Shigeki; Shimokake, Yoshiyuki; Nagata, Kiyoshi

LOCATION: Shinogi Research Laboratories, Shinogi & Co., Ltd., Osaka,

Japan, 553

JOURNAL: Eur. J. Biochem. DATE: 1996 VOLUME: 242 NUMBER: 3 PAGES:

460-466 COMMENT: EMBORI ISSN: 0014-2956 LANGUAGE: English PUBLISHER:

Springer

2/3,K/4 (Item 4 from file: 399)

DIAGNOSE File 399:CA SEARCH(E)

(c) 2002 American Chemical Society. All rts. reserv.

120316986 CA: 120(25)316986p JOURNAL

Cloning of rat Sertoli cell follicle-stimulating hormone primary response

complementary deoxyribonucleic acid: regulation of TSC-22 gene expression

AUTHOR(S): Hamill, Katherine G.; Hall, Susan H.

LOCATION: Dep. Pediatrics, Univ. North Carolina, Chapel Hill, NC, 27599,

USA

JOURNAL: Endocrinology DATE: 1994 VOLUME: 134 NUMBER: 3 PAGES:





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(C) 2003 The HM Wilson Co  
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(C) Format only 2003 The Dialog Group  
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(C) 2003 CAB International  
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(C) 2003 Reed Business Information Ltd.  
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(C) 1999 AAAS  
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(C) 2003 American Chemical Society  
File 434-SciSearch(E) Dated Ref Sci 1974-1989/Dec  
(C) 1996 Inst for Sci Info  
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(C) 2003 Elsevier Eng. Inform Ino  
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(C) 2003 Newsex  
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(C) 2003 NIS, Intl Copyright All Rights Res  
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(C) 2003 Thomson Datacom & ISI  
File 358-Derwent Biotech Abs 1987-2003 Dec  
(C) 2003 DECHENK  
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(C) Format only 2003 Dialog Corporation  
File 164-INTL JOURNAL OF MEDICAL RESEARCH 1964-2003 /Jan  
(C) 2003 BMJ  
File 447-AHA Journals 1967-2003 May B1  
(C) 2003 Amer Med Assn - PARS-DAYS apply  
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File 135: NewsRx Weekly Reports 1985-2003/Feb W1

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File 35: Dissertation Abs Online 1961-2003-Jan

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processing.

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See Items Description

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25 TSC22 (S) W472

Processing

Processing

Processing 10 of 38 files

Processing 20 of 38 files

Processing

Processing 20 of 38 files

Processing

Processing 20 of 38 files

Completed processing all files

20 TSC22

18910788 RATT

S1 4 TSC22 (S) RATT

2nd

Completed examining records

S2 4 RD (unique items)

280w files, 28,4/3, K all

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 File 162: CAB Health 1984-2003/ Jan  
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 File 370: Science 1996-1999/ Oct W2  
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22	35	12.4	85995	52	AC025715	Chondrichthys
23	36	12.4	125919	77	HE019615	Acipenser
24	35	12.4	156997	10	AC011465	Acipenser
25	36	12.4	172239	58	AC069587	Acipenser
26	36	12.4	182997	59	AC075031	Acipenser
27	36	12.4	219997	29	AC090415	Acipenser
28	35	12.4	299981	29	AC090492	Acipenser
29	34.6	12.3	179843	70	AF001272	Acipenser
30	34.6	12.3	185537	48	AF011263	Acipenser
31	34.6	12.3	152715	67	AF160258	Acipenser
32	34.1	12.2	95380	53	AF026770	Acipenser
33	34.4	12.2	98942	7	F2475	Acipenser
34	34.1	12.2	160335	58	AF064519	Acipenser
35	34.1	12.2	166636	42	AF020585	Acipenser
36	34.4	12.2	168839	52	AF025537	Acipenser
37	34.4	12.2	184789	49	AF020892	Acipenser
38	34.2	12.1	177976	68	AF156142	Acipenser
39	34.2	12.1	187919	67	AF162730	Acipenser
40	34	12.1	989932	48	HE128822	Acipenser
41	33.8	12.0	7219	81	AF6494	Human
42	33.8	12.0	46192	76	AF031125	Human
43	33.8	12.0	108685	66	AF157483	Human
44	33.8	12.0	156631	77	HE21236	Human
45	33.8	12.0	195910	8	AC095013	Human

## ALIGNMENTS

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VERSION  
KEYWORDS  
SOURCE  
ORGANISM

FASTA22A 1666 bp cDNA complete cds.  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1 (bases 1 to 1666)  
AUTHORS Hamik, K. and Hall, S.  
TITLE Cloning of rat Sertoli cell follicle stimulating hormone primary response complementary deoxyribonucleic acid. J Biol Chem 269: 1597-22  
JOURNAL Biol Cell 134 (3): 1295-1312 (1994)  
MEDLINE 94164020  
FEATURES  
SOURCE

FASTA22A 1666 bp cDNA complete cds.  
DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
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Query Match	91.9% Score 359.2; DB 11; Length 1666;			
Best Local Similarity	92.8%; Score No. 470-72;			
Matches 279; Mismatches 47; Indels 47; Gaps 11				

1666 bp cDNA complete cds.  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1 (bases 1 to 1666)  
AUTHORS Hamik, K. and Hall, S.  
TITLE Cloning of rat Sertoli cell follicle stimulating hormone primary response complementary deoxyribonucleic acid. J Biol Chem 269: 1597-22  
JOURNAL Biol Cell 134 (3): 1295-1312 (1994)  
MEDLINE 94164020  
FEATURES  
SOURCE

FASTA22A 1666 bp cDNA complete cds.  
DEFINITION  
ACCESSION  
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KEYWORDS  
SOURCE  
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[illegible]

444 : em hit q2 : \*  
 445 : em hit q3 : \*  
 446 : em dom s : \*  
 447 : qto fol s : \*  
 448 : qto fol s : \*  
 449 : qto hit q3 : \*  
 450 : qto hit q3 : \*  
 451 : qto hit q3 : \*  
 452 : qto hit q3 : \*

444	em	ht q 2 ; *
445	em	ht q 3 ; *
446	em	hdm 5 ; *
447	qto	pl 3 ; *
448	qto	pl 5 ; *
449	qto	ht q 6 ; *
450	qto	ht q 9 ; *
451	qto	ht q 10 ;
452	qto	ht q 11 ;
453	qto	ht q 12 ;

4.4.4:	$\sigma_{11}$	$\text{int } \sigma_{1,2}^*$	$\star$
4.4.5:	$\sigma_{10}$	$\text{int } \sigma_{1,5}^*$	$\star$
4.4.6:	$\sigma_{10}$	$\text{int } \sigma_{1,6}^*$	$\star$
4.4.7:	$\sigma_{10}$	$\text{int } \sigma_{1,7}^*$	$\star$
4.4.8:	$\sigma_{10}$	$\text{int } \sigma_{1,8}^*$	$\star$
4.4.9:	$\sigma_{10}$	$\text{int } \sigma_{1,9}^*$	$\star$
4.5.0:	$\sigma_{10}$	$\text{int } \sigma_{1,10}^*$	$\star$
4.5.1:	$\sigma_{10}$	$\text{int } \sigma_{1,11}^*$	$\star$
4.5.2:	$\sigma_{10}$	$\text{int } \sigma_{1,12}^*$	$\star$
4.5.3:	$\sigma_{10}$	$\text{int } \sigma_{1,13}^*$	$\star$
4.5.4:	$\sigma_{10}$	$\text{int } \sigma_{1,14}^*$	$\star$
4.5.5:	$\sigma_{10}$	$\text{int } \sigma_{1,15}^*$	$\star$
4.5.6:	$\sigma_{10}$	$\text{int } \sigma_{1,16}^*$	$\star$
4.5.7:	$\sigma_{10}$	$\text{int } \sigma_{1,17}^*$	$\star$

[illegible]

4.1.1	com	ht-q.2.5	*
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4.1.3	com	ht-q.4.5	*
4.1.4	com	ht-q.5.5	*
4.1.5	com	ht-q.6.5	*
4.1.6	com	ht-q.7.5	*
4.1.7	com	ht-q.8.5	*
4.1.8	com	ht-q.9.5	*
4.1.9	com	ht-q.10.5	*
4.1.10	com	ht-q.11.5	*
4.1.11	com	ht-q.12.5	*
4.1.12	com	ht-q.13.5	*
4.1.13	com	ht-q.14.5	*
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4.1.15	com	ht-q.16.5	*
4.1.16	com	ht-q.17.5	*
4.1.17	com	ht-q.18.5	*
4.1.18	com	ht-q.19.5	*
4.1.19	com	ht-q.20.5	*
4.1.20	com	ht-q.21.5	*
4.1.21	com	ht-q.22.5	*
4.1.22	com	ht-q.23.5	*
4.1.23	com	ht-q.24.5	*
4.1.24	com	ht-q.25.5	*
4.1.25	com	ht-q.26.5	*
4.1.26	com	ht-q.27.5	*
4.1.27	com	ht-q.28.5	*
4.1.28	com	ht-q.29.5	*
4.1.29	com	ht-q.30.5	*
4.1.30	com	ht-q.31.5	*
4.1.31	com	ht-q.32.5	*
4.1.32	com	ht-q.33.5	*
4.1.33	com	ht-q.34.5	*
4.1.34	com	ht-q.35.5	*
4.1.35	com	ht-q.36.5	*
4.1.36	com	ht-q.37.5	*
4.1.37	com	ht-q.38.5	*
4.1.38	com	ht-q.39.5	*
4.1.39	com	ht-q.40.5	*
4.1.40	com	ht-q.41.5	*
4.1.41	com	ht-q.42.5	*
4.1.42	com	ht-q.43.5	*
4.1.43	com	ht-q.44.5	*
4.1.44	com	ht-q.45.5	*
4.1.45	com	ht-q.46.5	*
4.1.46	com	ht-q.47.5	*
4.1.47	com	ht-q.48.5	*
4.1.48	com	ht-q.49.5	*
4.1.49	com	ht-q.50.5	*
4.1.50	com	ht-q.51.5	*
4.1.51	com	ht-q.52.5	*
4.1.52	com	ht-q.53.5	*
4.1.53	com	ht-q.54.5	*
4.1.54	com	ht-q.55.5	*
4.1.55	com	ht-q.56.5	*
4.1.56	com	ht-q.57.5	*
4.1.57	com	ht-q.58.5	*
4.1.58	com	ht-q.59.5	*
4.1.59	com	ht-q.60.5	*
4.1.60	com	ht-q.61.5	*
4.1.61	com	ht-q.62.5	*
4.1.62	com	ht-q.63.5	*
4.1.63	com	ht-q.64.5	*
4.1.64	com	ht-q.65.5	*
4.1.65	com	ht-q.66.5	*
4.1.66	com	ht-q.67.5	*
4.1.67	com	ht-q.68.5	*
4.1.68	com	ht-q.69.5	*
4.1.69	com	ht-q.70.5	*
4.1.70	com	ht-q.71.5	*
4.1.71	com	ht-q.72.5	*
4.1.72	com	ht-q.73.5	*
4.1.73	com	ht-q.74.5	*
4.1.74	com	ht-q.75.5	*
4.1.75	com	ht-q.76.5	*
4.1.76	com	ht-q.77.5	*
4.1.77	com	ht-q.78.5	*
4.1.78	com	ht-q.79.5	*
4.1.79	com	ht-q.80.5	*
4.1.80	com	ht-q.81.5	*
4.1.81	com	ht-q.82.5	*
4.1.82	com	ht-q.83.5	*
4.1.83	com	ht-q.84.5	*
4.1.84	com	ht-q.85.5	*
4.1.85	com	ht-q.86.5	*
4.1.86	com	ht-q.87.5	*
4.1.87	com	ht-q.88.5	*
4.1.88	com	ht-q.89.5	*
4.1.89	com	ht-q.90.5	*
4.1.90	com	ht-q.91.5	*
4.1.91	com	ht-q.92.5	*
4.1.92	com	ht-q.93.5	*
4.1.93	com	ht-q.94.5	*
4.1.94	com	ht-q.95.5	*
4.1.95	com	ht-q.96.5	*
4.1.96	com	ht-q.97.5	*
4.1.97	com	ht-q.98.5	*
4.1.98	com	ht-q.99.5	*
4.1.99	com	ht-q.100.5	*

4.1:	com	lit q 2.5 *
4.2:	com	lit q 3.5 *
4.3:	com	lit q 4.5 *
4.4:	com	lit q 5.5 *
4.5:	com	lit q 6.5 *
4.6:	com	lit q 7.5 *
4.7:	com	lit q 8.5 *
4.8:	com	lit q 9.5 *
4.9:	com	lit q 10.5 *
4.10:	com	lit q 11.5 *
4.11:	com	lit q 12.5 *
4.12:	com	lit q 13.5 *
4.13:	com	lit q 14.5 *
4.14:	com	lit q 15.5 *
4.15:	com	lit q 16.5 *
4.16:	com	lit q 17.5 *
4.17:	com	lit q 18.5 *
4.18:	com	lit q 19.5 *
4.19:	com	lit q 20.5 *
4.20:	com	lit q 21.5 *
4.21:	com	lit q 22.5 *
4.22:	com	lit q 23.5 *
4.23:	com	lit q 24.5 *
4.24:	com	lit q 25.5 *
4.25:	com	lit q 26.5 *
4.26:	com	lit q 27.5 *
4.27:	com	lit q 28.5 *
4.28:	com	lit q 29.5 *
4.29:	com	lit q 30.5 *
4.30:	com	lit q 31.5 *
4.31:	com	lit q 32.5 *
4.32:	com	lit q 33.5 *
4.33:	com	lit q 34.5 *
4.34:	com	lit q 35.5 *
4.35:	com	lit q 36.5 *
4.36:	com	lit q 37.5 *
4.37:	com	lit q 38.5 *
4.38:	com	lit q 39.5 *
4.39:	com	lit q 40.5 *
4.40:	com	lit q 41.5 *
4.41:	com	lit q 42.5 *
4.42:	com	lit q 43.5 *
4.43:	com	lit q 44.5 *
4.44:	com	lit q 45.5 *
4.45:	com	lit q 46.5 *
4.46:	com	lit q 47.5 *
4.47:	com	lit q 48.5 *
4.48:	com	lit q 49.5 *
4.49:	com	lit q 50.5 *
4.50:	com	lit q 51.5 *
4.51:	com	lit q 52.5 *
4.52:	com	lit q 53.5 *
4.53:	com	lit q 54.5 *
4.54:	com	lit q 55.5 *
4.55:	com	lit q 56.5 *
4.56:	com	lit q 57.5 *
4.57:	com	lit q 58.5 *
4.58:	com	lit q 59.5 *
4.59:	com	lit q 60.5 *
4.60:	com	lit q 61.5 *
4.61:	com	lit q 62.5 *
4.62:	com	lit q 63.5 *
4.63:	com	lit q 64.5 *
4.64:	com	lit q 65.5 *
4.65:	com	lit q 66.5 *
4.66:	com	lit q 67.5 *
4.67:	com	lit q 68.5 *
4.68:	com	lit q 69.5 *
4.69:	com	lit q 70.5 *
4.70:	com	lit q 71.5 *
4.71:	com	lit q 72.5 *
4.72:	com	lit q 73.5 *
4.73:	com	lit q 74.5 *
4.74:	com	lit q 75.5 *
4.75:	com	lit q 76.5 *
4.76:	com	lit q 77.5 *
4.77:	com	lit q 78.5 *
4.78:	com	lit q 79.5 *
4.79:	com	lit q 80.5 *
4.80:	com	lit q 81.5 *
4.81:	com	lit q 82.5 *
4.82:	com	lit q 83.5 *
4.83:	com	lit q 84.5 *
4.84:	com	lit q 85.5 *
4.85:	com	lit q 86.5 *
4.86:	com	lit q 87.5 *
4.87:	com	lit q 88.5 *
4.88:	com	lit q 89.5 *
4.89:	com	lit q 90.5 *
4.90:	com	lit q 91.5 *
4.91:	com	lit q 92.5 *
4.92:	com	lit q 93.5 *
4.93:	com	lit q 94.5 *
4.94:	com	lit q 95.5 *
4.95:	com	lit q 96.5 *
4.96:	com	lit q 97.5 *
4.97:	com	lit q 98.5 *
4.98:	com	lit q 99.5 *
4.99:	com	lit q 100.5 *
5.00:	com	lit q 101.5 *
5.01:	com	lit q 102.5 *
5.02:	com	lit q 103.5 *
5.03:	com	lit q 104.5 *
5.04:	com	lit q 105.5 *
5.05:	com	lit q 106.5 *
5.06:	com	lit q 107.5 *
5.07:	com	lit q 108.5 *
5.08:	com	lit q 109.5 *
5.09:	com	lit q 110.5 *
5.10:	com	lit q 111.5 *
5.11:	com	lit q 112.5 *
5.12:	com	lit q 113.5 *
5.13:	com	lit q 114.5 *
5.14:	com	lit q 115.5 *
5.15:	com	lit q 116.5 *
5.16:	com	lit q 117.5 *
5.17:	com	lit q 118.5 *
5.18:	com	lit q 119.5 *
5.19:	com	lit q 120.5 *
5.20:	com	lit q 121.5 *
5.21:	com	lit q 122.5 *
5.22:	com	lit q 123.5 *
5.23:	com	lit q 124.5 *
5.24:	com	lit q 125.5 *
5.25:	com	lit q 126.5 *
5.26:	com	lit q 127.5 *
5.27:	com	lit q 128.5 *
5.28:	com	

4.4:	com	hw 4.2.1	
4.5:	com	hw 4.2.1	
4.6:	com	hw 4.5 *	
4.7:	cd	hw 4.5 *	
4.8:	cd	hw 4.5 *	
4.9:	cd	hw 4.6.2 *	
5.0:	cd	hw 4.6.2 *	
5.1:	cd	hw 4.6.2 *	
5.2:	cd	hw 4.6.2 *	
5.3:	cd	hw 4.6.2 *	
5.4:	cd	hw 4.6.2 *	
5.5:	cd	hw 4.6.2 *	
5.6:	cd	hw 4.5 *	
5.7:	cd	hw 4.5 *	
5.8:	cd	hw 4.5 *	
5.9:	cd	hw 4.5 *	
6.0:	com	hw 4.5 *	
6.1:	com	hw 4.5 *	
6.2:	com	hw 4.5 *	
6.3:	com	hw 4.5 *	
6.4:	com	hw 4.5 *	
6.5:	cd	hw 4.5 *	
6.6:	cd	hw 4.5 *	

4.4:	com	lit	3.8	*
4.5:	com	lit	3.8	*
4.6:	com	lit	3.8	*
4.7:	ab	lit	3.8	*
4.8:	ab	lit	3.8	*
4.9:	ab	lit	3.8	*
5.0:	ab	lit	3.9	*
5.1:	ab	lit	4.1	*
5.2:	ab	lit	4.2	*
5.3:	ab	lit	4.4	*
5.4:	ab	lit	4.5	*
5.5:	ab	lit	4.8	*
5.6:	ab	lit	4.8	*
5.7:	ab	lit	4.7	*
5.8:	ab	lit	4.7	*
5.9:	ab	lit	4.7	*
6.0:	com	lit	4.4	*
6.1:	com	lit	4.5	*
6.2:	com	lit	4.5	*
6.3:	com	lit	4.7	*
6.4:	com	lit	4.8	*
6.5:	ab	lit	4.8	*
6.6:	ab	lit	4.9	*
6.7:	ab	lit	4.9	*
6.8:	ab	lit	4.7	*
6.9:	ab	lit	4.7	*

4.4:	com	hw	3.8	*
4.5:	com	hw	3.8	*
4.6:	com	hw	3.8	*
4.7:	sb	pl	3.8	*
4.8:	sb	hw	3.8	*
4.9:	sb	hw	3.8	*
5.0:	sb	hw	3.8	*
5.1:	sb	hw	3.8	*
5.2:	sb	hw	3.8	*
5.3:	sb	hw	3.8	*
5.4:	sb	hw	3.8	*
5.5:	sb	hw	3.8	*
5.6:	sb	hw	3.8	*
5.7:	sb	hw	3.8	*
5.8:	sb	hw	3.8	*
5.9:	sb	hw	3.8	*
6.0:	com	hw	3.8	*
6.1:	com	hw	3.8	*
6.2:	com	hw	3.8	*
6.3:	com	hw	3.8	*
6.4:	com	hw	3.8	*
6.5:	sb	hw	3.8	*
6.6:	sb	hw	3.8	*
6.7:	sb	hw	3.8	*
6.8:	sb	hw	3.8	*
6.9:	sb	hw	3.8	*
7.0:	sb	hw	3.8	*
7.1:	sb	hw	3.8	*

4.4:	com	hw	q.2.2. *
4.5:	com	hw	q.2.2. *
4.6:	com	hw	q.2.2. *
4.7:	sb	hw	q.2.2. *
4.8:	sb	hw	q.2.2. *
4.9:	sb	hw	q.2.2. *
5.0:	sb	hw	q.2.2. *
5.1:	sb	hw	q.2.2. *
5.2:	sb	hw	q.2.2. *
5.3:	sb	hw	q.2.2. *
5.4:	sb	hw	q.2.2. *
5.5:	sb	hw	q.2.2. *
5.6:	sb	hw	q.2.2. *
5.7:	sb	hw	q.2.2. *
5.8:	sb	hw	q.2.2. *
5.9:	sb	hw	q.2.2. *
6.0:	com	hw	q.2.2. *
6.1:	com	hw	q.2.2. *
6.2:	com	hw	q.2.2. *
6.3:	com	hw	q.2.2. *
6.4:	com	hw	q.2.2. *
6.5:	sb	hw	q.2.2. *
6.6:	sb	hw	q.2.2. *
6.7:	sb	hw	q.2.2. *
6.8:	sb	hw	q.2.2. *
6.9:	sb	hw	q.2.2. *
7.0:	sb	hw	q.2.2. *
7.1:	sb	hw	q.2.2. *
7.2:	sb	hw	q.2.2. *

Result	No.	Score	Unit	Match	Length	DB	ID
1	259	2	91.9	1.66	11	KAL1522	22
2	175	4	62.2	1.26	11	M0156	22
3	114	2	40.5	1.718	78	H5045604	60
4	114	2	40.5	1.725	78	H515661	60
5	114	2	40.5	1.65164	66	AL13918	66
6	114	2	40.5	1.455765	67	AL13918	66
7	91	0	7.2	0.1	0	AB37566	66
8	90	4	52.1	4.45	48	AB37566	66
9	69	8	24.8	1.61	4	AB37566	66
10	37	4	15.3	9.78	4	AB012462	42
11	36	4	12.9	5.51	11	MUS1C1	42
12	36	4	12.9	6.485	5	AB07606	42
13	36	4	12.9	1.656279	59	AB076275	42
14	36	4	12.9	1.90057	59	AB076275	42
15	36	2	12.8	2.03181	11	AB076288	42
16	36	4	12.8	1.1222	11	AB076288	42
17	36	4	12.8	1.19448	59	AB076288	42
18	36	4	12.8	1.43328	8	AB076288	42
19	36	4	12.8	1.65507	58	AB076288	42
20	36	4	12.6	1.19537	8	AB076288	42
21	36	4	12.4	1.2591	82	AB076288	42

is the number of

Year	March	Fourth	Day
1913	1465		
1914	1506		
1915	1718		
1916	1725		
1917	1651	654	
1918	548	753	
1919	732		
1920	485		
1921	1461	978	
1922	5831		
1923	6278		
1924	1527		
1925	1960	77	
1926	2041	118	
1927	11222		
1928	1511	1222	
1929	1645	208	
1930	1540	47	
1931	429	991	























117: em\_estp15:\*

118: em\_estp17:\*

119: em\_estp18:\*

120: em\_estp14:\*

121: em\_estp15:\*

122: em\_estp16:\*

123: em\_estp17:\*

124: em\_estp18:\*

125: em\_estp19:\*

126: qb\_est15:\*

127: qb\_est159:\*

128: qb\_est160:\*

129: qb\_est161:\*

130: qb\_est162:\*

131: qb\_est163:\*

132: qb\_est164:\*

133: qb\_est165:\*

134: qb\_est166:\*

135: qb\_est175:\*

136: qb\_est176:\*

137: qb\_est177:\*

138: qb\_est178:\*

139: qb\_est179:\*

140: qb\_est180:\*

141: qb\_est181:\*

142: qb\_est182:\*

143: qb\_est183:\*

144: qb\_est184:\*

145: qb\_est185:\*

146: qb\_est186:\*

147: qb\_est187:\*

148: qb\_est188:\*

149: qb\_est189:\*

150: qb\_est190:\*

151: qb\_est191:\*

152: qb\_est192:\*

153: qb\_est193:\*

154: qb\_est194:\*

155: qb\_est195:\*

156: qb\_est196:\*

157: qb\_est197:\*

158: qb\_est198:\*

159: qb\_est199:\*

160: qb\_est200:\*

161: qb\_est201:\*

162: qb\_est202:\*

163: qb\_est203:\*

164: qb\_est204:\*

165: qb\_est205:\*

166: qb\_est206:\*

167: qb\_est207:\*

168: qb\_est208:\*

169: qb\_est209:\*

170: qb\_est210:\*

171: qb\_est211:\*

172: qb\_est212:\*

173: qb\_est213:\*

174: qb\_est214:\*

175: qb\_est215:\*

176: qb\_est216:\*

177: qb\_est217:\*

178: qb\_est218:\*

179: qb\_est219:\*

180: qb\_est220:\*

181: qb\_est221:\*

182: qb\_est222:\*

183: qb\_est223:\*

184: qb\_est224:\*

185: qb\_est225:\*

186: qb\_est226:\*

187: qb\_est227:\*

188: qb\_est228:\*

189: qb\_est229:\*

190: qb\_est230:\*

190: qb\_est25:\*

191: qb\_est26:\*

192: qb\_est27:\*

193: qb\_est28:\*

Free: Results: The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SEQUENCES

Result No.	Score	Match	Length	DB	ID	Description
1	271.4	90.6	600	96	AW919433	AW919433 EST150737
2	270.8	90.6	516	26	AW919433	AW919433 EST150737
3	269.4	90.1	613	91	AW919433	AW919433 EST150737
4	269.4	90.0	851	4	AA274096	AA274096 SWMP-A191
5	266.2	89.0	605	13	AA870949	AA870949 ZG4805.1
6	265.4	88.8	285	10	AA684891	AA684891 EST105704
7	265.4	88.8	614	147	W64911	W64911 me07310.1
8	265.4	89.5	435	146	W64911	W64911 me07310.1
9	262.4	87.8	789	29	AA079988	AA079988 A079988
10	261.4	87.4	307	10	AA686663	AA686663 EST110964
11	261.4	87.4	447	104	BE126831	BE126831 DEFA0579
12	261.2	87.4	631	14	AA430314	AA430314 me18012.1
13	261.2	87.4	553	14	AA870869	AA870869 ZG4805.1
14	260.6	87.2	521	9	AA650671	AA650671 v171007.1
15	260.4	87.1	493	110	BE624163	BE624163 me24107.1
16	260.4	87.1	505	110	BE624199	BE624199 me24111.1
17	260.4	87.1	577	1	AA058143	AA058143 me52406.1
18	260.4	87.1	588	1	AA051753	AA051753 me54810.1
19	260.4	87.1	616	2	AA108589	AA108589 me44107.1
20	260.4	87.1	667	2	AA111757	AA111757 me51106.1
21	259.4	86.8	595	109	BE553384	BE553384 me51106.1
22	259.4	86.8	603	3	AA171174	AA171174 me44107.1
23	259.4	86.8	746	146	W13502	W13502 me44107.1
24	259.4	86.8	553	7	AA467396	AA467396 me52406.1
25	258.4	86.4	722	1	AA230311	AA230311 me52406.1
26	258.4	86.4	651	14	AA870869	AA870869 ZG4805.1
27	258.4	86.4	655	119	BE528197	BE528197 me44107.1
28	257.4	86.1	420	7	AA445291	AA445291 me52406.1
29	257.4	86.1	583	146	W13502	W13502 me44107.1
30	257.4	86.1	608	147	W13502	W13502 me44107.1
31	257.2	86.0	549	47	AA591875	AA591875 me52406.1
32	257.2	86.0	637	49	AA521413	AA521413 me52406.1
33	254	84.9	417	141	BE68887	BE68887 me44107.1
34	254	84.9	795	1	AA115272	AA115272 me44107.1
35	252.4	84.4	507	48	AA715279	AA715279 me44107.1
36	252.4	84.4	600	11	AA020218	AA020218 me50804.1
37	251.8	84.2	554	11	AA756067	AA756067 me44107.1
38	251.4	84.1	559	3	AA184150	AA184150 me44107.1
39	250.4	83.7	520	1	AA059780	AA059780 me74008.1
40	250.4	83.7	603	147	W13502	W13502 me44107.1
41	250	83.6	821	22	AA155715	AA155715 me44107.1
42	249.4	83.2	512	10	AA648327	AA648327 me44107.1
43	248.8	83.2	561	10	AA648327	AA648327 me44107.1
44	248.4	83.1	527	3	AA218198	AA218198 me52406.1
45	248.4	83.1	541	4	AA288533	AA288533 me52406.1

## ALIGNMENTS

RESULT 1

AW919433 600 bp mRNA

EST 25 MAY 2000

DIFFERENCE EST150737 Ref: Acc: F000000000

RELATIONSHIP: EST150737 Ref: Acc: F000000000

ACCESSION AW919433

VERSION AW919433.1

KEYWORDS EST

SOURCE Notway rat











[illegible]

RESULT 14  
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LOCUS AF253417 5272 bp. US6 Euk 25 MAY 2000

DEFINITION Homo sapiens mitochondrial epoxide hydrolase (EPHX1) gene, complete cds.

ACCESSION AF253417.229766.1.25880

VERSION AF253417.1 GI:8050709

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Artiodactyla; Primates; Hominidae; Homo.  
Mammalia; Euphrasia; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 9006 to 34795)  
Hassett, C., Poltsios, K. H., Peck, N. R. and Demopoulos, I. T.  
The human mitochondrial epoxide hydrolase gene (EPHX1): complete  
nucleotide sequence and structural characterization.  
Genomics 23 (2), 437-442 (1994)

JOURNAL MEDLINE  
951475940

PubMed 7835893

REFERENCE 2 (bases 1 to 15195)  
Hassett, C., Smith, J. M. and Omiecinski, C. J.  
5' flanking region of the human mitochondrial epoxide hydrolase gene,  
EPHX1  
Unpublished  
4 (bases 1 to 34795)  
Hassett, C., Alchor, L., Sidhu, J. S. and Omiecinski, C. J.  
Direct Submission  
Submitted (13-SEP-1994) Environmental Health, University of  
Washington, 4225 Roosevelt Way NE, Suite #100, Seattle, WA 98105,  
USA  
4 (bases 1 to 34795)  
Hassett, C., Smith, J. M. and Omiecinski, C. J.  
Direct Submission  
Submitted (12-MAY-2000) Environmental Health, University of  
Washington, 4225 Roosevelt Way NE, Suite #100, Seattle, WA 98105,  
USA

REMARK  
COMMENT  
FEATURES  
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Sequence update by submitter  
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* 208 2982: contig of 2695 bp in length
* 208 2982: gap of 100 bp
* 2483 6012: contig of 4530 bp in length
* 6113 6112: gap of 100 bp
* 6113 10247: contig of 4135 bp in length
* 10248 10347: gap of 100 bp
* 10348 15153: contig of 4806 bp in length
* 15154 15253: gap of 100 bp
* 15254 21342: contig of 6189 bp in length
* 21343 21542: gap of 100 bp
* 21543 26581: contig of 5039 bp in length
* 26582 26681: gap of 100 bp
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* 125641 146684: contig of 21044 bp in length
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* 108 287: gap of 100 bp
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* 21543 26581: contig of 5039 bp in length
* 26582 26681: gap of 100 bp
* 26682 33499: contig of 6814 bp in length
* 33499 33598: gap of 100 bp
* 33599 39935: contig of 6536 bp in length
* 39936 40035: gap of 100 bp
* 40036 48266: contig of 8215 bp in length
* 48267 48366: gap of 100 bp
* 48367 58440: contig of 10074 bp in length
* 58441 58540: gap of 100 bp
* 58541 67465: contig of 8925 bp in length
* 67466 67565: gap of 100 bp
* 67566 77575: contig of 10010 bp in length
* 77576 77675: gap of 100 bp
* 77676 91864: contig of 14189 bp in length
* 91865 91964: gap of 100 bp
* 91965 106970: contig of 15006 bp in length
* 106971 107070: gap of 100 bp
* 107071 125540: contig of 18470 bp in length
* 125541 125640: gap of 100 bp
* 125641 146684: contig of 21044 bp in length
* 146685 146784: gap of 100 bp
* 146785 171941: contig of 25157 bp in length

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## FEATURES

## SOURCE

1. 171941

/organism "Homo sapiens"

/db\_xref "taxon:9606"

/chromosome "X"

/map "X"

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/feature "11b "REF1 11 Human Male 10A"

1. 171941

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/feature "assembly Treatment"

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/feature "assembly Treatment"

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/feature "assembly Treatment"

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/feature "assembly Treatment"

26582 26681

/feature "assembly Treatment"

26682 33499

/feature "assembly Treatment"

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* 33499 33598: gap of 100 bp
* 33599 39935: contig of 6536 bp in length
* 39936 40035: gap of 100 bp
* 40036 48266: contig of 8215 bp in length
* 48267 48366: gap of 100 bp
* 48367 58440: contig of 10074 bp in length
* 58441 58540: gap of 100 bp
* 58541 67465: contig of 8925 bp in length
* 67466 67565: gap of 100 bp
* 67566 77575: contig of 10010 bp in length
* 77576 77675: gap of 100 bp
* 77676 91864: contig of 14189 bp in length
* 91865 91964: gap of 100 bp
* 91965 106970: contig of 15006 bp in length
* 106971 107070: gap of 100 bp
* 107071 125540: contig of 18470 bp in length
* 125541 125640: gap of 100 bp
* 125641 146684: contig of 21044 bp in length
* 146685 146784: gap of 100 bp
* 146785 171941: contig of 25157 bp in length

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Contract : Sequence Submissions 'spnagow.wt.mut.cedu'  
Project Information  
Contract project name: L11124  
Contract name: 609 E.18

• Note: This record contains all the roads that  
• sequencing roads that have not been assembled into  
• contigs. Roads of N are used to separate the roads  
• and the order in which they appear is completely  
• arbitrary. Low pass sequence sampling is useful for  
• identifying clones that may be over-represented and allow  
• overlap relationships among clones to be detected.  
• However, it should not be assumed that this clone  
• will be sequenced to completion. In the event that  
• the record is updated, the accession number will  
• be preserved.

• 743 842: gap of 100 bp in length  
• 843 1568: contig of 716 bp in length  
• 1569 1658: gap of 100 bp  
• 1659 2001: contig of 743 bp in length  
• 2002 2491: gap of 100 bp  
• 2492 4292: contig of 711 bp in length  
• 4293 4602: gap of 100 bp  
• 4603 4641: contig of 749 bp in length  
• 4642 4731: gap of 100 bp  
• 4732 4815: contig of 762 bp in length  
• 4816 4963: gap of 100 bp  
• 4964 5000: contig of 747 bp in length  
• 5001 5790: gap of 100 bp  
• 5791 5842: contig of 752 bp in length  
• 5843 6042: gap of 100 bp  
• 6043 7478: contig of 746 bp in length  
• 7479 8192: contig of 714 bp in length  
• 8193 8292: gap of 100 bp  
• 8293 9011: contig of 719 bp in length  
• 9012 9111: gap of 100 bp  
• 9112 9651: contig of 740 bp in length  
• 9652 9951: gap of 100 bp  
• 9952 10675: contig of 724 bp in length  
• 10676 10775: gap of 100 bp  
• 10776 11490: contig of 721 bp in length  
• 11491 11566: gap of 100 bp  
• 11567 12411: contig of 745 bp in length  
• 12412 12441: gap of 100 bp  
• 12442 13202: contig of 761 bp in length  
• 13203 13802: gap of 100 bp  
• 13803 14583: contig of 748 bp in length  
• 14584 14750: gap of 100 bp  
• 14751 14878: contig of 728 bp in length  
• 14879 14978: gap of 100 bp  
• 14979 15715: contig of 747 bp in length  
• 15716 15815: gap of 100 bp  
• 15816 16545: contig of 745 bp in length  
• 16547 16645: gap of 100 bp  
• 16647 17474: contig of 728 bp in length  
• 17475 17474: gap of 100 bp  
• 17475 18204: contig of 740 bp in length  
• 18205 18404: gap of 100 bp  
• 18405 19025: contig of 721 bp in length  
• 19026 19125: gap of 100 bp  
• 19126 19843: contig of 718 bp in length  
• 19844 19943: gap of 100 bp  
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• 20663 20762: gap of 100 bp  
• 20763 21475: contig of 743 bp in length  
• 21476 21565: gap of 100 bp  
• 21566 22348: contig of 743 bp in length  
• 22349 22481: gap of 100 bp  
• 22490 23100: contig of 746 bp in length  
• 23101 23200: gap of 100 bp  
• 23201 23975: contig of 689 bp in length

• 23976 24075: gap of 100 bp  
• 24076 24814: contig of 749 bp in length  
• 24815 24914: gap of 100 bp  
• 24915 25640: contig of 746 bp in length  
• 25641 25790: gap of 100 bp  
• 25791 26477: contig of 727 bp in length  
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• 26578 27429: contig of 752 bp in length  
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• 46499 47212: contig of 744 bp in length  
• 47213 47312: gap of 100 bp  
• 47313 48028: contig of 716 bp in length  
• 48029 48128: gap of 100 bp  
• 48129 48865: contig of 727 bp in length  
• 48866 48955: gap of 100 bp  
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• 49676 49775: gap of 100 bp  
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• 51421 52169: contig of 749 bp in length  
• 52170 52269: gap of 100 bp  
• 52270 53005: contig of 746 bp in length  
• 53006 53105: gap of 100 bp  
• 53106 53847: contig of 742 bp in length  
• 53848 53947: gap of 100 bp







C 22	31.4	19.9	160964	47	AC019419	Homo sapi
C 23	31.2	19.8	1471	11	FNRS8A	Y1319.9 Homo sapi
C 24	31.2	18.8	179855	65	AC079446	AC079446, pathogen
C 25	31.2	18.8	194129	59	AC073741	AC073741, Homo sapi
C 25	31.1	18.6	206435	41	AC015236	A1159340, Homo sapi
C 26	31	18.7	3219	8	AC024334	AB024334, Homo sapi
C 26	31	18.7	3747	9	AC011339	AF011339, Homo sapi
C 29	31	18.7	67995	65	AC080112	AC080112, Homo sapi
C 30	31	18.7	148619	9	AC066812	AC066812, Homo sapi
C 31	31	18.7	157717	38	AC010336	AC010336, Homo sapi
C 32	31	18.7	169489	30	AC010188	AC010188, Homo sapi
C 33	31	18.7	179865	57	AC068297	AC068297, Homo sapi
C 34	31	18.7	173787	55	AC046135	AC046135, Homo sapi
C 35	30.9	18.6	93349	37	AL113422	AL113422, Homo sapi
C 36	30.8	18.6	106816	84	HSS171M3	Contribution (4 of
C 37	30.9	18.6	159594	50	AC052440	AC052440, Homo sapi
C 38	30.8	18.6	169930	40	AC015914	AC015914, Homo sapi
C 39	30.8	18.6	188240	49	AC021541	AC021541, Homo sapi
C 40	30.8	18.6	201129	38	AC011368	AC011368, Homo sapi
C 41	30.8	18.6	206161	40	AC015915	AC015915, Homo sapi
C 42	30.8	18.6	209816	68	AL356130	AL356130, Homo sapi
C 43	30.8	18.6	210136	84	HE93110	AL113442, Homo sapi
C 44	30.6	18.6	340000	77	HS210202	AL165392, Homo sapi
C 45	30.6	18.4	184904	11	MM01738347	A1223837, Homo sapi

## ALIGNMENTS

AC015812	Homo sapi
AF024426	Homo sapi
AF074476	Homo sapi
AF077741	Mus muscu
AF115180	Homo sapi
AF024164	Homo sapi
AF024166	Homo sapi
AF060818	Homo sapi
AC001336	Homo sapi
AC001088	Homo sapi
AC068297	Homo sapi
AC094135	Homo sapi
AF173102	Homo sapi
Continuation of	
AC025440	Homo sapi
AC015914	Homo sapi
AC002154	Homo sapi
AC011358	Homo sapi
AC015915	Mus muscu
AF135130	Homo sapi
AF133402	Homo sapi
AF165309	Homo sapi
AF152837	Mus muscu

RESULT	1
DI7447	
LOCUS	D17447 3410 bp mRNA ROD 04-FEB-1999
DEFINITION	Rattus norvegicus mRNA for 14-3-3 protein, gamma-subtype, complete cds.
ACCESSION	D17447
VERSION	D17447.1 GI:402525
KEYWORDS	14-3-3 protein, gamma-subtype, regulation of protein kinase C, Rattus norvegicus (strain:Wistar) postnatal day 21 brain cDNA, cDNA, mRNA.
SOURCE	Rattus norvegicus
ORGANISM	Fukushima, Matsuo, Chouda, Vothelstra, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
REFERENCE	1 (bases 1 to 3410)
AUTHORS	Watanabe, M.
TITLE	Direct Submission
JOURNAL	Submitted (14 Aug 1993) to the EMBL/GenBank databases
	Department of Anatomy, Hokkaido University School of Medicine, Faculty of Anatomy, Nishi-15 Kita-7, Kita-ku, Sapporo 060, Jpn (Tel:011-17-11330, Fax:011-717-5286)
REFERENCE	2 (bases 1 to 3410)
AUTHORS	Watanabe, M., Isebe, T., Ichimura, T., Kuroda, R., Takakashi, Y. and Kondo, H.
TITLE	Molecular cloning of rat cDNAs for beta and gamma subtypes of 14-3-3 protein and developmental changes in expression of their mRNAs in the nervous system
JOURNAL	Brain Res. Mol. Brain Res. 17 (1-2), 135-146 (1993)
MEDLINE	93164855
REFERENCE	3 (bases 1 to 3410)
AUTHORS	Watanabe, M., Isebe, T., Ichimura, T., Kuroda, R., Takakashi, Y., Kondo, H. and Inoue, Y.
TITLE	Molecular cloning of rat cDNAs for the alpha and beta subtypes of 14-3-3 protein and differential distributions of their mRNAs in the brain
JOURNAL	Brain Res. Mol. Brain Res. 25 (1-2), 113-121 (1994)
MEDLINE	95075241
FEATURES	Location/Qualifiers
source	1..3410

[illegible][illegible]

GenView Version 4.5  
Copyright (c) 1993-2000 CompuLink Ltd.

OR nucleotide nucleotide search, using sw model

Run on: April 11, 2001, 18:02:55 Search time 4464.91 Seconds

(601000 alignment(s))  
190.272 Mbits per cell updates/sec

Files: 09:49 490-609b-488

Footest scores: 166  
1: reversed and reversed ..... approach of alignment 166

Scoring table: IDENTITY: 100, gapext: 1.0

Searches: 118633 steps, 2558875100 positions

Total number of hits satisfying chosen parameters: 226266

Minimum OR seq length: 0

Maximum OR seq length: 200000000

Best processing: Minimum Match: 0K

Maximum Match: 100K

Listed first 45 summaries

Database: 1: gb\_ba1.1  
2: gb\_ba2.1  
3: gb\_cmg.1  
4: gb\_ey.1  
5: gb\_pbl.1  
6: gb\_pbl.2  
7: gb\_pbl.3  
8: gb\_pbl.4  
9: gb\_pbl.5  
10: gb\_pbl.6  
11: gb\_pbl.7  
12: gb\_pbl.8  
13: gb\_pbl.9  
14: gb\_pbl.10  
15: gb\_pbl.11  
16: gb\_pbl.12  
17: gb\_pbl.13  
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19: gb\_pbl.15  
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45: gb\_pbl.41

Result No.	Score	Query Match	Length	DB ID	Description
1	140	84.3	4410	11	D17447
2	140	84.3	4410	11	S55405
3	85.2	51.3	198701	65	A0083753
4	64.4	20.7	164494	10	A020898
5	44	20.5	672224	65	A0080050
6	44	20.5	69260	55	A0084877
7	44	20.5	191573	39	A012486
8	42.8	19.8	180490	58	A0069152
9	42.8	19.4	97916	77	HS30822
10	42.6	19.6	206059	59	A0074312
11	42.6	19.5	226059	65	A0079488
12	42.6	19.6	243275	59	A0074705
13	42.4	19.5	52358	77	HS27610
14	42.4	19.5	171941	53	A0026531
15	42.4	19.5	175170	66	A0084815
16	42.4	19.4	166504	54	A0044779
17	42.2	19.3	181029	58	A0059978
18	41.8	19.3	190000	29	A0007108
19	41.8	19.2	208818	65	A0079644
20	41.8	19.2	178710	10	A0011477
21	41.4	18.9	166978	8	A0004098

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Thu Apr 12 10:22:21 2001

us-09-490-609b-318.rni

Page 8











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1  NUMBER OF SEQUENCES: 4
2  ADDRESS/PHONE ADDRESS:
3  ADDRESS: 400 West Colorado Boulevard, Suite 500
4  STREET: 400 West Colorado Boulevard, Suite 500
5  CITY: Pasadena
6  STATE: California
7  COUNTRY: United States
8  ZIP: 91105
9  COMPUTER REWARD FORM:
10 MEDIUM TYPE: Floppy disk
11 OPERATING SYSTEM: pc DOS/MS-DOS
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: 08/09/92, 434
14 FILING DATE: 17 Dec 1992
15 CLASSIFICATION: 435
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 08/09/92, 752
18 FILING DATE: 24 Dec 1992
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/09/92, 430
21 FILING DATE: 12 MAR 1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/09/92, 434
24 FILING DATE: 13 MAR 1992
25 ADDRESS/PHONE ADDRESS:
26 NAME: Fred, L. Brown
27 REGISTRATION NUMBER: 20058
28 REFERENCE/SEQUENCE NUMBER: 08/09/92, 4379
29 TELEPHONE: (626) 795 9900
30 TELEFAX: (626) 797 8800
31 INFORMATION: 435
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 524 base pairs
34 TYPE: nucleic acid
35 SUBSTANCE: both
36 MEDIUM TYPE: DNA (Genomic)
37 US OR 992 344 2
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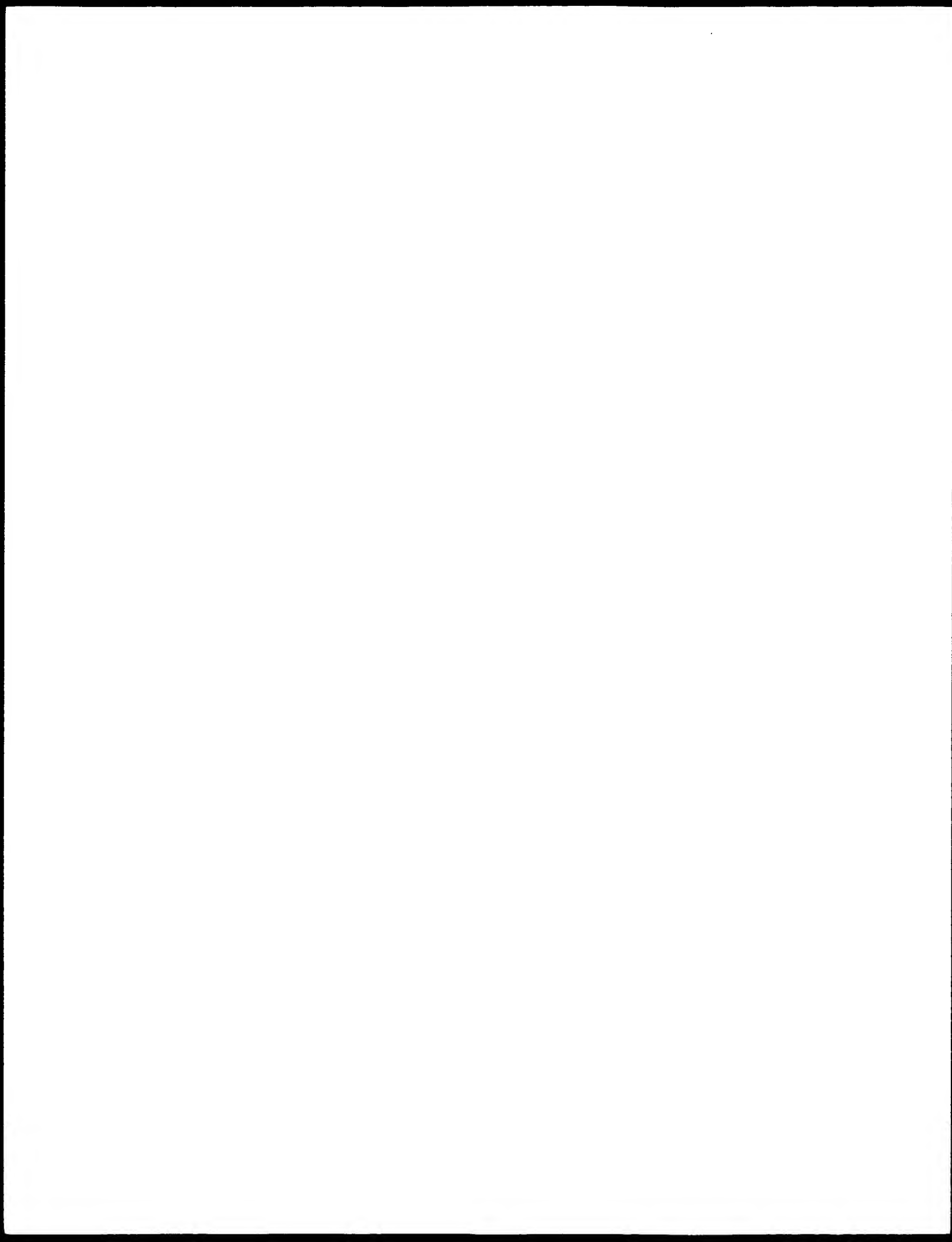
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Access DB# 39471

# SEARCH REQUEST FORM

Scientific and Technical Information Center

*[Signature]*

Requester's Full Name: \_\_\_\_\_  
Art Unit: \_\_\_\_\_  
Phone Number 30 \_\_\_\_\_  
Serial Number: \_\_\_\_\_  
Examiner #: \_\_\_\_\_  
Date: \_\_\_\_\_  
Results Format Preferred (circle): PAPER DISK E-MAIL  
Mail Box and Bldg/Room Location: \_\_\_\_\_

If more than one search is submitted, please prioritize searches in order of need.  
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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or unity of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
Inventors (please provide full names): \_\_\_\_\_

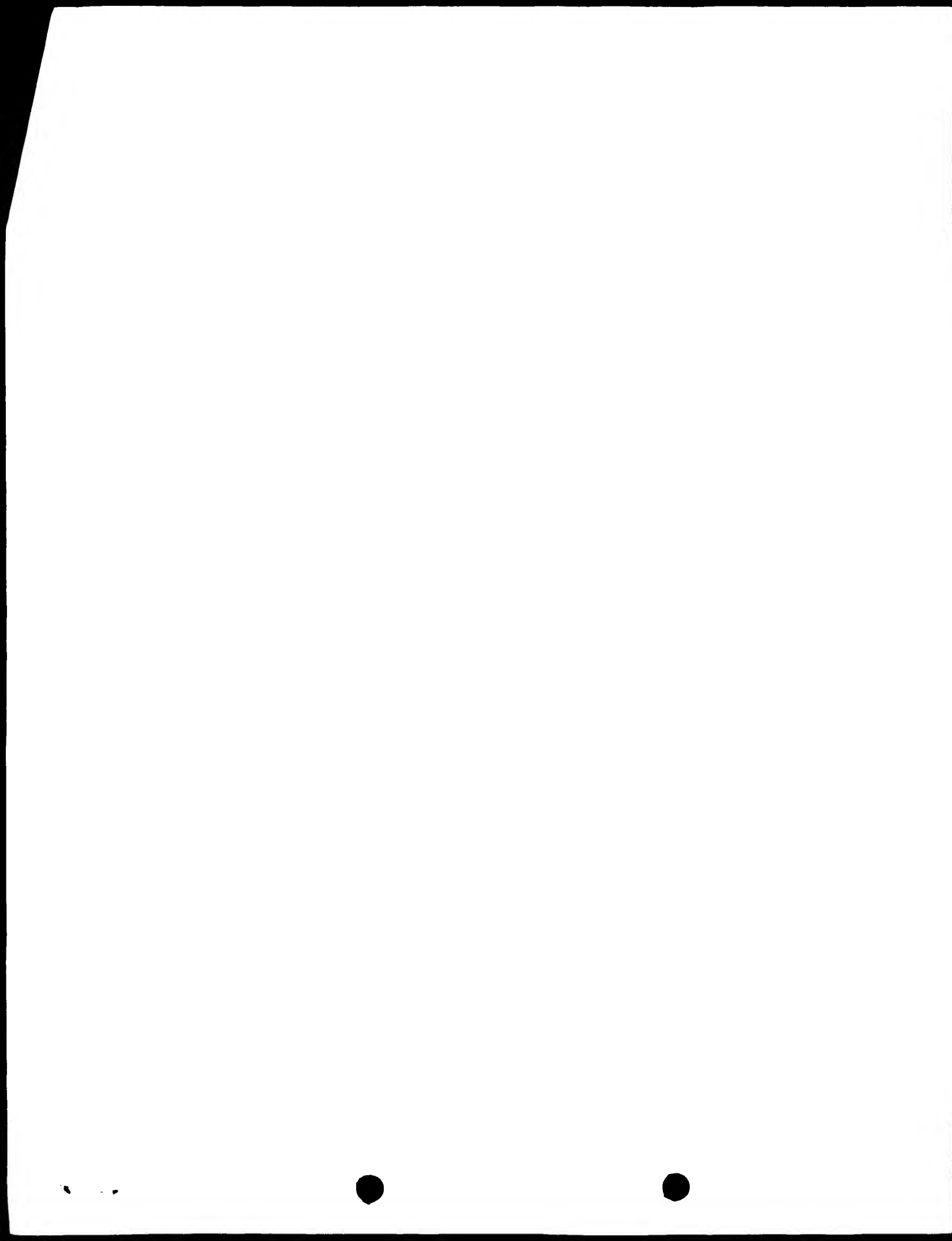
Earliest Priority Filing Date: \_\_\_\_\_  
\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Vendors and cost where applicable

\*\*\*\*\*

STAFF USE ONLY

STAFF USE ONLY  
Searcher: *Edmond - July*  
Searcher Phone #: *308-4801*  
Searcher Location: *Box 261*  
Date Searcher Picked Up: *4/9/01*  
Date Completed: *4/13/01*  
Searcher Prep & Review Time: *8 min*  
Clerical Prep Time: *3 min*  
Online Time: \_\_\_\_\_  
Type of Search: *7*  
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AA Sequence (#) \_\_\_\_\_  
Structure (#) \_\_\_\_\_  
Bibliographic \_\_\_\_\_  
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Sequence Systems *AB5501*  
WWW/Internet \_\_\_\_\_  
Other (specify) \_\_\_\_\_



STIC-Biotech/ChemLib

39491

CRF

From:  
Sent:  
To:  
Subject:

Lacourciere, Karen  
Friday, April 06, 2001 3:37 PM  
STIC-Biotech/ChemLib  
Sequence Search 09/490,609

Please search the following sequences for 09/490609 in both the commercial databases and the inference database:

SEQ ID NO: 317, 318, 280, 337, 465, 488, and 384.

Thank-you!

Karen A. Lacourciere Ph.D.  
CM1 11D09 GAU 1635  
(703) 308-7523





The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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OTHER INFORMATION: unsure at all n locations  
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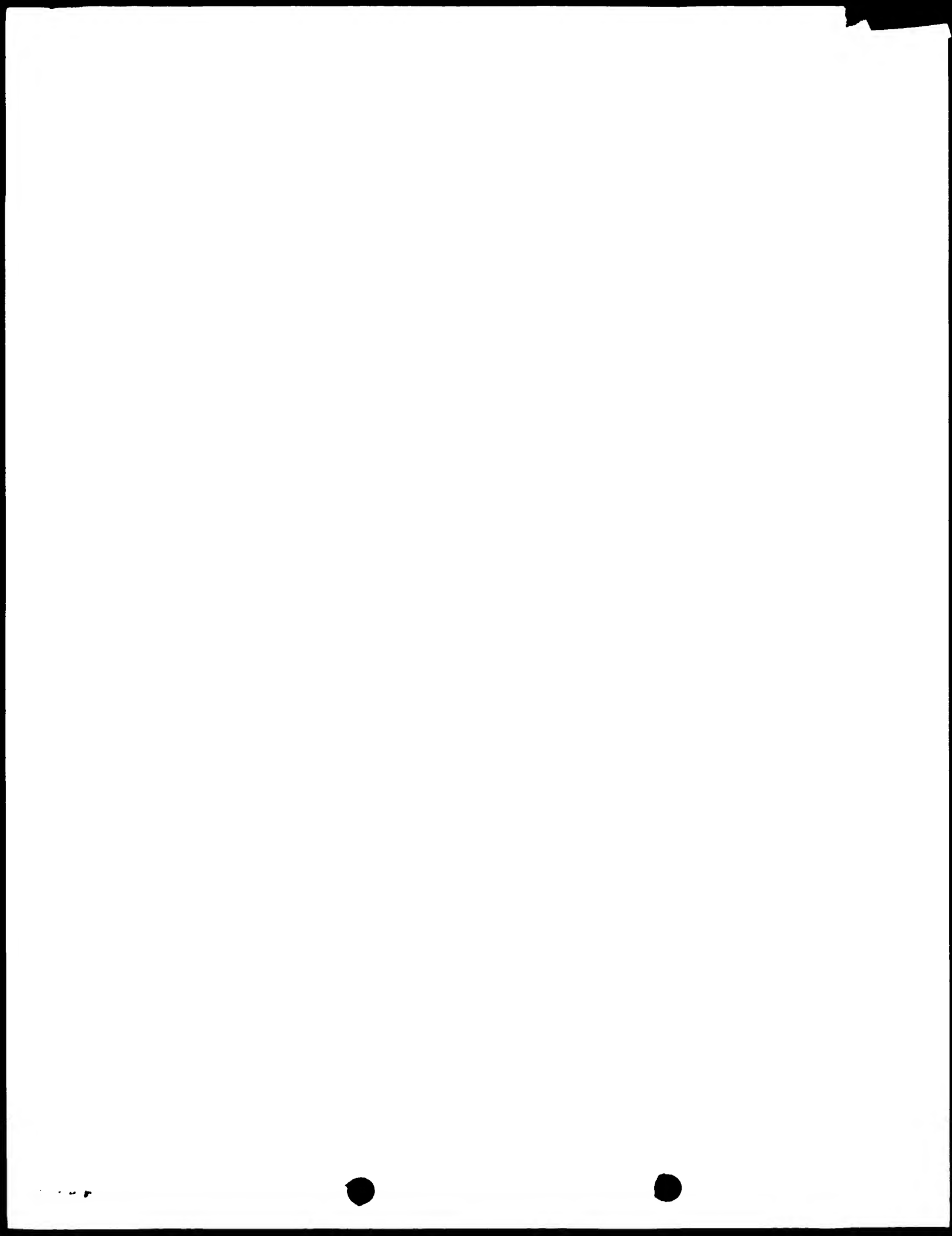
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 File 164: Allied & Complementary Medicine 1984-2001/Aug  
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S2	97610	CANCER? (W) (MARKER? OF DIAGNOS?)
S3	347300	NEOPLAS? (W) (MARKER? OF DIAGNOS?)
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S11	0	RD (unique items)
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 65:Inside Conferences 1993-2001/Aug WI  
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 73:EMBASE 1974-2001 Jul M5  
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Thu Apr 12 10:22:41 2001

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 REFERENCE 1 Liu M.Y., Kuroda, J., Lacey, M., Lau, F., Mullins, J., Morris, M., Schellhammer, K., Stephens, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R., and Watson, R. The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: HMI Project  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (401) 406-1459  
 Email: Robert.Strausberg@nih.gov  
 Tissue procurement: Gilbert Smith, Ph.D.  
 cDNA library preparation: Life Technologies, Inc.  
 cDNA library arrayed by: The I.M.A.C.E. Consortium (LIM)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.C.E. Consortium/LIM at:  
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 providing samples: Gilbert Smith, NIH  
 BASE COUNT 119 a 144 c 138 g 176 t  
 ORIGIN  
 Query Match 49.4% Score 82. Lip 107. Length 577.  
 Best Local Similarity 75.6% Pred. No. 120-141  
 Matches 127 Conservative 0 Mismatches 47 Indels 4 Gaps 2  
 VERSION AA770737  
 DEFINITION 5012941207 Mammalian Hem1 5Kp cDNA clone  
 ACCESSION AA770737  
 VERSION AA770737.1 GI:3469529  
 KEYWORDS EST  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 (bases 1 to 577)  
 REFERENCE 1 Liu M.Y., Kuroda, J., Lacey, M., Lau, F., Mullins, J., Morris, M., Schellhammer, K., Stephens, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R., and Watson, R. The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: HMI Project  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (401) 406-1459  
 Email: Robert.Strausberg@nih.gov  
 Tissue procurement: Gilbert Smith, Ph.D.  
 cDNA library preparation: Life Technologies, Inc.  
 cDNA library arrayed by: The I.M.A.C.E. Consortium (LIM)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.C.E. Consortium/LIM at:  
<http://image.jim.scripps.edu/>  
 Plates: LIM8765 row: h column: 03  
 High quality sequence stop: 574  
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 Library: constructed by Life Technologies, Inc. at the University of California, San Diego, CA  
 providing samples: Gilbert Smith, NIH  
 BASE COUNT 119 a 144 c 138 g 176 t  
 ORIGIN

LOCUS BR77714 577 bp mRNA EST 21 JUL 2000  
 DEFINITION 5012941207 Mammalian Hem1 5Kp cDNA clone IMAGE594197  
 ACCESSION BR77714  
 VERSION BR77714.1 GI:5422189  
 KEYWORDS EST  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 (bases 1 to 577)  
 REFERENCE 1 Liu M.Y., Kuroda, J., Lacey, M., Lau, F., Mullins, J., Morris, M., Schellhammer, K., Stephens, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R., and Watson, R. The WashU-HMI Mouse EST Project  
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 COMMENT Contact: HMI Project  
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 Plates: LIM8765 row: h column: 03  
 High quality sequence stop: 574  
 FEATURES  
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 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE359338"  
 /cotton\_lib="NCI-CCAF-Mam1"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, vitelline"  
 /lab\_host="DH10B"  
 /host="gamma, manure"; Vector: pCMV-SPECK, Stratagene, La Jolla, CA  
 Library: constructed by Life Technologies, Inc. at the University of California, San Diego, CA  
 providing samples: Gilbert Smith, NIH  
 BASE COUNT 119 a 144 c 138 g 176 t  
 ORIGIN  
 Query Match 48.4% Score 80.2 Lip 29. Length 271.  
 Best Local Similarity 74.8% Pred. No. 47-141  
 Matches 141 Conservative 0 Mismatches 49 Indels 4 Gaps 2  
 VERSION AA770737  
 DEFINITION 5012941207 Mammalian Hem1 5Kp cDNA clone  
 ACCESSION AA770737  
 VERSION AA770737.1 GI:2822548  
 KEYWORDS EST  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 (bases 1 to 294)  
 REFERENCE 1 Liu M.Y., Kuroda, J., Lacey, M., Lau, F., Mullins, J., Morris, M., Schellhammer, K., Stephens, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R., and Watson, R. The WashU-HMI Mouse EST Project  
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 COMMENT Contact: HMI Project  
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 Plates: LIM8765 row: h column: 03  
 High quality sequence stop: 574  
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 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, vitelline"  
 /lab\_host="DH10B"  
 /host="gamma, manure"; Vector: pCMV-SPECK, Stratagene, La Jolla, CA  
 Library: constructed by Life Technologies, Inc. at the University of California, San Diego, CA  
 providing samples: Gilbert Smith, NIH  
 BASE COUNT 94 a 63 c 54 g 65 t  
 ORIGIN  
 Query Match 48.4% Score 80.2 Lip 29. Length 271.  
 Best Local Similarity 74.8% Pred. No. 47-141  
 Matches 141 Conservative 0 Mismatches 49 Indels 4 Gaps 2  
 VERSION AA770737  
 DEFINITION 5012941207 Mammalian Hem1 5Kp cDNA clone  
 ACCESSION AA770737  
 VERSION AA770737.1 GI:2822548  
 KEYWORDS EST  
 SOURCE house mouse  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 (bases 1 to 294)  
 REFERENCE 1 Liu M.Y., Kuroda, J., Lacey, M., Lau, F., Mullins, J., Morris, M., Schellhammer, K., Stephens, M., Tan, F., Underwood, K., Moore, B., Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R., and Watson, R. The WashU-HMI Mouse EST Project  
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<http://image.jim.scripps.edu/>  
 Plates: LIM8765 row: h column: 03  
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 FEATURES  
 source  
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 /db\_xref="taxon:10090"  
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 /host="gamma, manure"; Vector: pCMV-SPECK, Stratagene, La Jolla, CA  
 Library: constructed by Life Technologies, Inc. at the University of California, San Diego, CA  
 providing samples: Gilbert Smith, NIH  
 BASE COUNT 94 a 63 c 54 g 65 t  
 ORIGIN

## ORGANISM

Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

1 (bases 1 to 97)

AUTHORS: Katsuyuki Matsuzawa, Toshiaki Saitoh, and Soichi M.B.

TITLE: Normalization and subtraction: two approaches to facilitate gene

expression

JOURNAL: Gene

1999; 244: 1709

COMMENT: Contact: Chao H National Institute of Medical Health

4001 Executive Blvd, Box 28, Rockville, MD 20852, USA

Tel: 301 443 1709

Fax: 301 443 1709

Email: mts@nih.gov

Note: This is a preprint of a manuscript with a modified

sequence. The NIH library is a subtracted library derived from

NIH 3T3 cells, which in turn is a subtracted library derived from

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## ACCESSION

IMAGE:162741.5, mRNA sequence

VERSION

A1592463.1 GI:4601511

KEYWORDS

EST

SOURCE

house mouse

ORGANISM

Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

1 (bases 1 to 460)

AUTHORS: Katsuyuki Matsuzawa, Toshiaki Saitoh, and Soichi M.B.

TITLE: Normalization and subtraction: two approaches to facilitate gene

expression

JOURNAL: Gene

1999; 244: 1709

COMMENT: Contact: Chao H National Institute of Medical Health

4001 Executive Blvd, Box 28, Rockville, MD 20852, USA

Tel: 301 443 1709

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Note: This is a preprint of a manuscript with a modified

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 118: em\_estp17:\*  
 119: em\_estp18:\*  
 120: em\_estp19:\*  
 121: em\_estp20:\*  
 122: em\_estp21:\*  
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 197: em\_estp96:\*  
 198: em\_estp97:\*  
 199: em\_estp98:\*  
 200: em\_estp99:\*  
 201: em\_estp100:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	83.6	50.4	497	39	AM047721	AM047721 01-M-BH1
2	81.2	50.1	466	22	AM047721	AM047721 01-M-BH1
3	81.2	49.4	577	107	HE372124	HE372124 00122 0312
4	80.2	48.8	271	28	AM014748	AM014748 AM014748
5	71	42.8	293	11	AA720737	AA720737 011102.1
6	69.10	40.4	1055	190	CNS00030	AM069499 1008 0011
7	63.6	20.2	1013	193	CNS01083	AM106871 1008 0011
8	62.6	13.8	1301	193	CNS00070	AM094287 1008 0011
9	62.6	19.6	449	89	AM261421	AM261421 00122 0312
10	62.2	19.4	529	100	AM272286	AM272286 00122 0312
11	62.2	19.4	518	40	AM164647	AM164647 00122 0312
12	62	19.4	560	40	AM157201	AM157201 00122 0312
13	61.6	19.0	1093	193	CNS00003	AM157201 00122 0312
14	61.6	19.0	1095	193	CNS00003	AM157201 00122 0312
15	61.6	18.9	748	192	CNS00003	AM157201 00122 0312
16	61.2	18.8	742	148	AM004857	AM004857 00122 0312
17	61.2	18.8	888	190	CNS00003	AM157201 00122 0312
18	61.2	18.8	949	192	CNS00003	AM157201 00122 0312
19	61	18.7	296	146	W23904	W23904 00122 0312
20	61	18.7	400	79	AM070701	AM070701 00122 0312
21	61	18.7	558	41	AA292187	AA292187 00122 0312
22	61.1	18.7	611	96	AM047750	AM047750 00122 0312
23	61.1	18.7	618	92	AM009940	AM009940 00122 0312
24	61.1	18.7	651	94	AM752806	AM752806 00122 0312
25	61	18.7	727	176	AM189404	AM189404 00122 0312
26	61	18.7	1194	149	HE045576	HE045576 00122 0312
27	60.8	18.6	507	111	HE045576	HE045576 00122 0312
28	60.8	18.6	546	93	AM050535	AM050535 00122 0312
29	60.8	18.6	555	135	HE070072	HE070072 00122 0312
30	60.8	18.6	893	137	HE070072	HE070072 00122 0312
31	60.8	18.6	922	139	CNS00074W	AM067784 00122 0312
32	60.8	18.6	991	192	CNS00074W	AM067784 00122 0312
33	60.8	18.6	125	142	HE045576	HE045576 00122 0312
34	60.6	18.4	432	15	AM1010612	AM1010612 00122 0312
35	60.6	18.4	466	108	HE042117	HE042117 00122 0312
36	60.6	18.4	469	192	CNS00003	AM157201 00122 0312
37	60.6	18.4	480	104	HE104725	HE104725 00122 0312
38	60.6	18.4	569	17	AM176034	AM176034 00122 0312
39	60.6	18.4	586	156	AM075005	AM075005 00122 0312
40	60.6	18.4	741	149	AM016005	AM016005 00122 0312
41	60.6	18.4	755	107	HE070072	HE070072 00122 0312
42	60.6	18.4	1047	109	HE045576	HE045576 00122 0312
43	60.4	18.3	308	10	AM057476	AM057476 00122 0312
44	60.4	18.3	440	178	AM292989	AM292989 00122 0312
45	60.3	18.3	576	183	AM509392	AM509392 00122 0312

## ALLEGMENTS

RESULT 1  
 AM047721  
 LOCUS  
 DEFINITION  
 C1 M-BH1 410 9 11 0 01:51 NHE-BH1 M-52 1000 basepairs cDNA clone  
 ACCESSION  
 AM047721  
 VERSION  
 AM047721.1 G1:5908250  
 KEYWORDS  
 EST  
 SOURCE  
 HOMO SAPIENS



190: qb\_gss25:\*  
191: qb\_gss26:\*  
192: qb\_gss27:\*  
193: qb\_gss28:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	184	63.7	448	17	A1170562	A1170562 EST216494
C 2	184	63.7	479	12	AA851056	AA851056 EST193824
C 3	184	63.7	480	24	A1713203	A1713203 UI-R-Y0-a
C 4	178.2	61.7	481	14	AA914539	AA914539 z202b02.f
C 5	172.8	59.8	502	4	AA268983	AA268983 z395d07.f
C 6	172.8	59.8	656	18	A12566412	A12566412 ui84107.x
C 7	172.8	59.8	683	26	A1875662	A1875662 uk51b08.x
C 8	172.8	59.8	692	26	A1875662	A1875662 uk51b08.x
C 9	172.8	59.8	709	138	BE980156	BE980156 UI-M-B02-
C 10	172.8	59.8	721	16	A1118166	A1118166 ue38f05.x
C 11	172.8	59.8	744	23	A1647488	A1647488 uk42a09.x
C 12	172.8	59.8	829	17	A1195553	A1195553 ui52a11.x
C 13	171.2	59.2	411	4	AA238092	AA238092 mx78e05.f
C 14	171.2	59.2	484	104	BE133018	BE133018 ui34a01.x
C 15	171.2	59.2	561	25	A1766994	A1766994 uj51b05.x
C 16	170.8	59.1	496	104	BE133649	BE133649 uk04a09.x
C 17	169.8	58.8	793	16	A1114891	A1114891 ui49f06.x
C 18	169.8	58.8	426	17	A1236567	A1236567 EST233129
C 19	167	57.8	411	94	AW741912	AW741912 ui97f03.y
C 20	167	57.8	523	7	AA422350	AA422350 vi45d08.f
C 21	166.4	57.6	570	94	AW701821	AW701821 ui45a05.x
C 22	166.4	57.6	629	91	AW702123	AW702123 uk98e02.x
C 23	164.8	57.0	436	104	BE133073	BE133073 ui34h08.x
C 24	164.8	57.0	503	16	A1159703	A1159703 ui03d11.x
C 25	164.8	57.0	543	17	A1194773	A1194773 ui56e05.x
C 26	163.2	56.5	487	104	BE132873	BE132873 ui47d01.x
C 27	162.2	56.1	208	15	A1035435	A1035435 ub46e11.x
C 28	161.6	55.9	592	18	A1303360	A1303360 ui77d08.x
C 29	156.8	54.3	390	108	BE449103	BE449103 ui52a02.y
C 30	150.2	52.0	401	29	A0042738	A0042738 A0042738
C 31	150	51.9	258	146	W18222	W18222 z359h04.f
C 32	149.8	51.8	510	111	BE649120	BE649120 UI-M-BH1-
C 33	139.6	48.3	390	22	A1575136	A1575136 UI-R-E0-C
C 34	135.2	46.9	383	13	AA900551	AA900551 UI-R-E0-C
C 35	134.8	46.6	394	108	BE447635	BE447635 ui52e02.x
C 36	134.4	46.5	379	4	AA250517	AA250517 mw9q03.f
C 37	131.6	45.5	382	17	A1181916	A1181916 ud77d02.x
C 38	131.6	45.5	394	39	AW047588	AW047588 UI-M-BH1-
C 39	127	43.9	624	97	AW964180	AW964180 EST376253
C 40	127	43.9	658	38	AV701709	AV701709 AV701709
C 41	127	43.9	683	38	AV703975	AV703975 AV703975
C 42	125.4	43.4	420	24	A1751826	A1751826 cn12b03.x
C 43	125.4	43.4	473	8	AA487871	AA487871 ab13b07.s
C 44	125	43.3	571	105	BE236194	BE236194 143894.MA
C 45	121.8	42.1	412	23	A1676208	A1676208 wc72d09.x

ALIGNMENTS

RESULT	1	A1170562	448 bp	mRNA	EST
LOCUS	EST216494	Normalized rat lung			20-JAN-1999
DEFINITION	RLUCQ81 3' end	mRNA sequence			Rattus sp. cDNA clone
ACCESSION	A1170562				
VERSION	EST				
KEYWORDS	Rattus sp.				
SOURCE					

```

cm_nucleic     nucleic search, using sw model
Run on:        April 11, 2001, 15:40:40 ; Search time 344.44 Seconds
               (without alignments)
               605,550 Million cell updates/sec

Title:         US-09-490-609b-337
Percent score: 289
Sequence:      1 at gaagatcttctatgcccac.....tggagaaattttttccccc 289

Scoring table:
IDENTITY: No
Gapop 10.0 , Gapext 1.0

Searched:     7991742 seqs, 450374058 residues
               15986484

Total number of hits satisfying chosen parameters:
Minimum hit seq length: 0
Maximum hit seq length: 2000000000

Post processing: Minimum Match 0%
                  Maximum Match 100%
                  List of 11st 45 summaries

Database:
1:  qb_est1 : *
2:  qb_est2 : *
3:  qb_est3 : *
4:  qb_est4 : *
5:  qb_est5 : *
6:  qb_est6 : *
7:  qb_est7 : *
8:  qb_est8 : *
9:  qb_est9 : *
10: qb_est10 : *
11: qb_est11 : *
12: qb_est12 : *
13: qb_est13 : *
14: qb_est14 : *
15: qb_est15 : *
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110: qb_est110 : *
111: qb_est111 : *
112: qb_est112 : *
113: qb_est113 : *
114: qb_est114 : *
115: qb_est115 : *
116: qb_est116 : *

```